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Sequence 8355, Ap
Sequence 102, Ap
Sequence 102, App
Sequence 273, App
Sequence 23894, A
Sequence 245, Ap
Sequence 245, Ap
Sequence 245, Ap
Sequence 38981, A
Sequence 38981, A
Sequence 38981, A
Sequence 38981, A
                                                                                                                               March 10, 2006, 18:48:35; Search time 544 Seconds (without alignments) 1615.956 Million cell updates/sec
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Sequence 496714,
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                                                                                                                                                                                                                                                     381 '
1 atggcgtcaaactcaagaag.....gttatattttctttggtttaa
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-096-568A-2919
US-11-096-568A-21894
US-11-096-568A-4492
US-11-096-568A-4492
US-11-096-568A-4492
US-10-714-887-245
US-10-750-185-38981
US-10-750-623-38981
US-10-750-623-38981
US-09-925-065A-64600
US-09-925-065A-96715
US-09-925-065A-96715
US-09-925-065A-96716
US-09-925-065A-94149
US-09-925-065A-944139
US-09-925-065A-944139
US-09-925-065A-944139
US-09-925-065A-948139
US-09-925-065A-948139
US-09-925-065A-986884
US-09-925-065A-9808884
US-09-925-065A-9808884
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Maximum Match 100%
Listing first 45 summaries
                                                                                        - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
TITLE OF INVENTION: Therby
FILE REPERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 8355
LENGTH: 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 CCCGACCGATGCCACAATGTGGCAAAAGCTGTCGGAGGGAAAACTGTAGAAGAAGTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 ccadacadereccacecreereccecececerecerecadadaaaaaceerecaaeaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 TGGACGTTTAGTCAAAACAAGATGTTCGAGAGGGCCTTGGCAGTTTACGACAAGGACACA
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                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
i LOCATION: (1)...(517)
cother Information: Ceres Seq. ID no. 15225172
US-11-096-568A-8355
Sequence 8355, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 25.77
Best Local Similarity 69.8
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                     ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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269

210 AGGCATTATGAGAAGCTCGTGGAAGATGTGAGGAGATTGAGGAAGGTCACGTGCCCTC

CCCAATTAC 222 |||||||||| CCCAATTAC 278

214

154 CGCCACTATGACATTCTCGTCGAGGATCTCATCAACATCGAGACTGGTCGTGTCCCTTTG

6 8 6

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OTHER INFORMATION: G1634; predicted polypeptide sequence is paralogous to G2701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 CAAGGACACACCCGACCGATGGCACAATGTGGCAAAAGCTGTCGGAGGGAAAACTGTAGA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 rearcacaccicarcaciderraaacticacrarcarcacacacacacarar
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24 AATCTCACCATGGACGTTTAGTCAAAACAAGATGTTCGAGAGGGCCTTGGCAGTTTACGA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2003-11-13

FRIOR LILING DATE: 2003-11-13

FRIOR FILING DATE: 2003-04-10

FRIOR FILING DATE: 2003-04-10

FRIOR FILING DATE: 2000-02-17

FRIOR FILING DATE: 1999-05-20

FRIOR FILING DATE: 1999-05-20

FRIOR PELING DATE: 1999-05-32

FRIOR FILING DATE: 2000-03-22

FRIOR FILING DATE: 2000-03-22

FRIOR FILING DATE: 2000-03-22

FRIOR PELING DATE: 2000-03-22

FRIOR APPLICATION NUMBER: 09/713, 994

FRIOR PELING DATE: 2000-11-16

FREMAINING PRIOR APPLICATION ADDITING DATE: 2000-11-16

FREMAINING PRIOR APPLICATION NUMBER: 09/713, 994

FROM SOFTWARE: PALENTIN VERSION 3.2

FROM SEQ ID NOS: 430

SEQ ID NOS: 500-011-16

FENGTH - 0.273

FENGTH - 0.273

FENGTH - 0.273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CANALES, ROGER
APPLICANT: REBETTI, Peter
APPLICANT: RUMIMOTO, Roderick W
APPLICANT: REUBER, T. Lynne
APPLICANT: REUBER, T. Lynne
APPLICANT: PINEDA, Omalia
APPLICANT: SHERNAN, Bradley K
TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF DROUGHT STRESS
FILE REFERENCE: MS10058-CIP
CURRENT APPLICATION NUMBER: 105/10/714,887
CURRENT FILING DATE: 2003-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gape
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58.3%; Pred. No. 9.3e-06;
iive 0; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Mendel Biotechnology, Inc. APPLICANT: HEARD, Jacqueline APPLICANT: RIECHMANN, Jose Luis APPLICANT: CREELMAN, Robert APPLICANT: RATCLIFFE, Oliver
                                                                                                                                                                                                                                                               US-10-714-887-273
; Sequence 273, Application US/10714887
; Publication No. US20060015972A1
; GENERAL INFORMATION:
                                                                                           205 GTCCCTTTGCCCAATTAC 222
                                                                                                                                                 280 GÍTCCGAÍTCCCGGCÍÁC 297
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Matches 116; Conserv
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                          US-11-096-568A-29719
Sequence 29719, Application US/11096568A
Fublication No. US20060048240A1
GENERAL INFORMATION:
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: 1 Therby
TITLE OF INVENTION: 2150-15920402
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 29719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 ACCCGACCGATGGCACAATGTGGCAAAAGCTGTCGGAGGGAAAACTGTAGAAGAAGTGAA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 recedacadarderecadadrecereceargerrecederadadererear 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 AAGGACACCCGACCGATGGCACAATGTGGCAAAAGCTGTCGGAGGGAAAACTGTAGAA 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 GCGCCACTATGACATTCTCGTCGAGGATCTCATCAACATCGAGACTGGTCGTGTCCCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 18.4%; Score 70; DB 9; Length 876
Best Local Similarity 60.5%; Pred. No. 1.3e-06;
Matches 115; Conservative 0; Mismatches 75; Indels
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Sequence 102, Application US/11087099

Publication No. US20060041961A1

GENERAL INFORMATION:

APPLICANT: Abad, Mark S. et al.

TILLE OF INVENTION: Genes and Uses for Plant Improvement;
FILE REFRENCE: 38-21(53450) EP

CURRENT APPLICATION NUMBER: US/11/087,099

CURRENT FILING DATE: 2005-03-22

NUMBER OF SEQ ID NOS: 12464

SEQ ID NO 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1). (376)
; OTTER INFORMATION: Ceres Seq. ID no. 4926979
US-11-096-568A-29719
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
SRGANISM: Arabidopsis thaliana
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Matches 116; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 CCCTGGTTAC 252
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; OTHER INFORMATION: G2701 reference sequence; predicted polypeptide sequence is par US-10-714-887-245
                                                                                                                                                                            85 AAGGACACACCCGACCGATGGCACAATGTGGCAAAAGCTGTCGGAGGGAAAACTGTAGAA 144
                                                                                                                                                                                                                          572 AGCACAAAATGGACCTCTGAAGAGAACAAGCTCTTTGAAAATGCTCTTGCAGTGCATGAT 631
                                                                                                                                                                                                                                                                                                                                            145 GAAGTGAAGCGCCACTATGACATTCTCGTCGAGGATCTCATCAACATCGAGACTGGTCGT 204
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APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: RECEMAN, Jacqueline
APPLICANT: RECEMAN, Jacqueline
APPLICANT: CANALES, Roger
APPLICANT: CANALES, Roger
APPLICANT: REPETTI, Peter
APPLICANT: RUMINOTO, Roderick W
APPLICANT: REBERS, T. Lynne
APPLICANT: SHERMAN, Bradley K
TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF DROUGHT STRESS
FILE REFERENCE: MBIO058-CIP
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NUMBER OF SEQ ID NOS: 430
SOFTWARE: Patentin version 3.2
SEQ ID NO 245
LENGTH: 866
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CURRENT FILING DATE: 2003-11-13

PRIOR APPLICATION NUMBER: US/10/112,699

PRIOR FILING DATE: 2003-04-10

PRIOR APPLICATION NUMBER: 09/506,720

PRIOR PILING DATE: 2000-02-17

PRIOR APPLICATION NUMBER: 09/135,134

PRIOR PILING DATE: 1999-05-20

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 2000-03-22

PRIOR PILING DATE: 2000-03-22

PRIOR PAPLICATION NUMBER: 09/533,029

PRIOR PELLING DATE: 2000-03-22

PRIOR PELLING DATE: 2000-03-32

PRIOR PELLING DATE: 2000-03-32

PRIOR PELLING DATE: 2000-03-32

PRIOR PELLING DATE: 1999-03-33
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PU52
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
LENGTH: 994
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Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INVERTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-15922US2
CURRENT APPLICATION VMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
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222 AGATGTCATGAGGCAATACTCTAAGCTTGAAGAAGACCTCTTCGATATCGAAGCAGGACT 281
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Best Local Similarity 56.9%; Pred. No. 5.1e-05;
Matches 116; Conservative 0; Mismatches 88; Indels
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; OTHER INFORMATION: Ceres Seq. ID no. 12416292
US-11-096-568A-23894
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; LOCATION: (1)..(1724)
; OTHER INFORMATION: Ceres Seq. ID no. 13638441
US-11-096-568A-4492
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23894, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
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                                                                                                                          204 TGTCCCTTTGCCCAATTAC 222
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ORGANISM: Zea mays subsp. mays
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US-11-096-568A-4492
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LENGTH: 1724
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2055 ACTCTAAATATCTAATAATCATTTAATAAATTTATCTTTCTGAGTTGAAATTTTTTG 2114
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                                                                                                                                                                                                                                                                                                                                                                  1995 ACTGAATATGTTTCATTGTAGATGTAAACAGGCAATTAACTAAAGTCATATTTCAGCCAG 2054
                                                                                                                                                                                                                                                                                                                           239 ACTCAAGAAGCATCAATGACTTTGACACAAGGTATATAACTAAATATCTATATATGATGC 298
                                                                                                                                                                                                                                                                                                                                                                                                                            299 TCTCGATATTTTTGATAATCATTCTAGTGATTTTTGAGAAATTCTCTCAAAAAGTTCTTG 358
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APPLICANT: RERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: APPLICATION WINDER: US/10/750,623
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR PILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE FELING AND STEPHEN OF SEQ ID NOS: 64922
SOFTWARE PARENTED NO SECOND OF SECOND NOS: 64922
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                                                                                                                                                                                                                   Score 42.6; DB 8; Length 2891;
Pred. No. 2.6;
0; Mismatches 59; Indels 0
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; Sequence 664600, Application US/09925065A
; Publication No. US20040181048A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 38981, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: MMI GENOMICS, Sue K.
APPLICANT: KERR, Richard
APPLICANT: KERR, Richard
APPLICANT: MOSEN
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ORGANISM: Bovine 19866881325079
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                                                                                                                               TYPE: DNA
ORGANISM: Bovine 19866881325079
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PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFWARE: Patentin version 3.1
SEQ ID NO 38981
LENGTH: 2891
                                                                                                                                                                                                                           Query Match
Best Local Similarity 56.9%;
Matches 78; Conservative
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Matches 78; Conservative
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US-10-750-623-38981
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LENGTH: 2891
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Sequence 21266, Application US/11096568A

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: 1592000
TITLE OF INVENTION: 2005-04-01
CURRENT FILING DATE: 2005-04-01
SEQ ID NOS: 34471
LENGTH: 1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 GAGGAGGTCAGGCGGCACTACGGGCTGCTGGTGGAGGACGACCGGCATCGAGTCGGGC 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 GAAGAAGTGAAGCGCCACTATGACATTCTCGAGGATCTCATCAACATCGAGACTGGT 201
                                                                                                                                                                                                           154 CGCCACTATGACATTCTCGTCGAGGATCTCATCAACATCGAGACTGGTCGTGTCCCTTTG 213
                                                                                                                                                                                                                                             262 AAGCAATATAGTAAGCTTGAAGACGTTTTCGATATTGAAGCAGGACGTGTTCCCATT 321
                                                                                                        CCCGACCGATGGCACAATGTGGCCAAAAGCTGTCGGAGGGGAAAAACTGTAGAAGAAGTGAAG 153
                                                                                                                                                         202 cergaredererakadrietrecardarecerdakadekeretririndarenara 261
                                                         TGGACGTTTAGTCAAAACAAGATGTTCGAGGGGCCTTGGCAGTTTACGACAAGGACACA
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Publication No. US20050260603A1
GENERAL INPORMATION:
APPLICANT: MAI GENONICS, INC.
APPLICANT: ROSENRELD, David
APPLICANT: ROSENRELD, David
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-2
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14.1%; Score 53.6; DB 9; Length 1254;
Best Local Similarity 59.0%; Pred. No. 0.007;
Matches 92; Conservative 0; Mismatches 64; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 CGTGTCCCTTTGCCCAATTACAAGACCTTCGAATCT 237
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; LOCATION: (1)._[1254)
; OTHER INFORMATION: Ceres Seq. ID no. 12402516
US-11-096-568A-21266
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CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
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ORGANISM: Zea mays subsp. mays
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                                                                                                                                                                                                                                                                                                              214 CCCAATTA 221
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US-10-750-185-38981
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258 TAAAAGACTATATATATATATATATATATATATATATAAATATATAAAWATATATATA 199
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Best Local Similarity 58.8
Matches 67; Conservative
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                                                                                                                                                                                                                                                                                                             371 CTTT 374
                                                                                                                                                                                                                                                                                                                                                                                                              138 TCTT 135
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TRNGTH: 590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 TCAATGACTTTGACACAAGGTATATAACTAAATATCTATATGATGATGCTCTCGATATT 310
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GENERAL INFURCATION:
GENERAL INFURCATION:
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: INCLEDIA NUCLECTION OF STREET OF INVENTION: NUCLECTION OF STREET OF ST
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Sequence 525531, Application US/09925065A

Publication No. US20040181048A1

GREERAL INPORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: NUCLECTION NUCLECTION NUCLECTION NUCLECTION OF STATE OF STA
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10.2%; Score 38.8; DB 6;
Best Local Similarity 56.5%; Pred. No. 13;
Matches 70; Conservative 1; Mismatches 53;
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Best Local Similarity 58.0°
Matches 69; Conservative
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US-09-925-065A-664600
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US-09-925-065A-525531/c
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LENGTH: 527
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ORGANISM:

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                                                                              198 TATATAAGCTGGGCAATTCTAAGGAAATTCAAACCAAAAAGTTGTGGCCAGTTAAATTA 139
311 ITGATAATCATTCTAGTGATTTTGAGAAATTCTCTCAAAAAGTTCTTGTAAGTTATATTT 370
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR PILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2001-13-0
PRIOR FILING DATE: 2001-13-0
PRIOR FILING DATE: 2001-13-0
PRIOR FILING DATE: 2001-13-0
PRIOR FILING DATE: 2001-01-16
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Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang Joyn G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 GCATCAATGACTTTGACACAAGGTATATAACTAAATATCTATATATGATGCTCTCGATAT 307
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US-09-925-065A-496716/C

is Sequence 496716/C

sequence 496716, Application US/09925065A

sequence 496716, Application US/09925065A

publication No. US20040181048A1

general INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Mucleotide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2000-10-80

PRIOR PILING DATE: 2000-10-24

PRIOR PILING DATE: 2000-11-20

PRIOR PELING DATE: 2000-11-30

PRIOR PILING DATE: 2000-11-30

PRIOR PELING DATE: 2000-11-30

PRIOR PELING DATE: 2001-01-16

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10.2%; Score 38.8; DB 6; Length 607;
Best Local Similarity 58.8%; Pred. No. 13;
Matches 67; Conservative 0; Mismatches 47; Indels (
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PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 495714
LENGTH: 607
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Job time : 546 secs
                                                                                                                                                                                                                             TYPE: DNA
CRGANISM: Homo sapiens
US-09-925-065A-496714
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US-09-925-065A-496716
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March 10, 2006, 18:46:11; Search time 573 Seconds (without alignments) 5498.487 Million cell updates/sec
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381
1 atggcgtcaaaactcaagaag.....gttatatttctttggtttaa
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
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7: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
1: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
GenCore vergion 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                             OM nucleic - nucleic search, using sw model
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seq length: 200000000
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Description	Sequence 1, Appli Sequence 1, Appli		271,	6644		4786,	13836,	16005,	1448	11476,	11563,	Sequence 5000, Ap	103390	473,	6	2719,	359, 7	5934,	Sequence 9298, Ap	5904,
ID	US-10-697-787-1 US-10-512-600-1	US-10-767-795-270	10-767-795-271	0-424-599-6644	US-10-425-114-14832 US-10-424-599-135729	10-260-238-	US-10-021-323-13836	US-10-021-323-16005	US-10-021-323-14482	-10-021-323-1	US-10-021-323-11563	US-10-767-795-5000	US-10-424-599-103390	US-09-770-152-473	10-225-066A-35	US-10-374-780A-2719	US-10-225-066A-359	US-10-767-795-5934	US-10-021-323-9298	US-10-424-599-5904
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Query Match Length	381	760	779	678	730	466	577	505	532	538	542	604	619	556	578	578	578	636	584	507
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Score	381	120.6	119	116.8	110.8	110	108.4	107.4	107.4	107.4	107.4	107.4	106	104.8	104.8	104.8	104.8	103.8	103.4	98.6

Result No.

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21 Sequence 9021, Ap Sequence 5644, A Sequence 61, Appl Sequence 16, Appl Sequence 16525, Sequence 16525, Sequence 2672, A Sequence 2672, A Sequence 39009, A Sequence 39009, A Sequence 13529, A Sequence 13529, A Sequence 13529, A Sequence 13529, A Sequence 13529, A Sequence 27843, A Sequence 27843, A Sequence 253, Appl Sequence 653, Appl Sequence 653, Appl Sequence 653, Appl Sequence 653, Appl Sequence 653, Appl Sequence 119, Appl Sequence 2679, Appl Sequence 2679, Appl Sequence 119, Appl Sequence 2679, Appl Sequence 119, Appl Sequence 119, Appl Sequence 97856, A Sequence 97856, A	ENTS s with Improved Pathogen Resistance and 87	8; Length 381; -94; 0; Indels 0; Gaps 0;	GACGITIAGICAAAACAAGAIGIIC 60 	GAGAGGCCTTGGCAGTTTACGACAGGACACACCCGACCGA	GCTGTCGGAGGAAAACTGTAGAAGAGAGGCCACTATGACATTCTCGTCGAGGAT 180 	CTCATCAACATCGAGACTGGTCGTGTCCCTTTGCCCAATTACAAGACCTTCGAATCTAAC 240 	TCAAGAAGCATCAATGACTTTGACACAAGGTATATAACTAAATATCTATATATGATGCTC 300 
507 7 US-10-425-114-9021 513 7 US-10-425-5642 513 7 US-10-425-5642 513 7 US-10-412-699B-61 732 8 US-10-697-781-18 732 8 US-10-425-115-16525 733 7 US-10-425-115-39009 742 7 US-10-425-115-39009 776 7 US-10-425-115-39009 776 7 US-10-425-115-39009 776 7 US-10-425-115-39009 776 7 US-10-021-323-13428 867 7 US-10-021-323-13428 867 9 US-10-021-323-13428 867 7 US-10-225-0664-653 867 7 US-10-225-0664-653 867 9 US-10-225-0664-653 881 8 US-10-425-115-97866 613 7 US-10-425-067-119	GNM 7,7 3333	100.0%; Score 381; DB 100.0%; Pred. No. 2.8e- ative 0; Mismatches	atgecetcaaactcaagaacttcaatctcaccatgeacetttagtcaaacaagatgtt 	rgcagtttacgacaaggacacacc 	ggada ctgtagaagaagtgaggg 	rcgagactggtcgtgtccctttgcc 	rcaatgactttgacacaaggtatat 
C 25 93 24.4 27 98.6 25.9 27 93.4 24.3 28 91.8 24.1 28 91.8 24.1 30 89.4 23.5 30 89.4 22.8 31 84.6 22.2 33 84.6 22.2 34 83.6 21.9 35 82.2 37 81.2 21.6 37 79.6 20.9 40 79.6 20.9 41 79.6 20.9 42 79.6 20.9 43 78.4 20.6 44 78.4 20.6	1 Applicatio NMATION: Agrinomics VENTION: MCE: AG03- LICATION WING CATION NUM G DATE: 20 CATION NUM G DATE: 20 CATION NUM G DATE: 20 ATABIGOBEI	Query Match Best Local Similarity Matches 381; Conservi	Qy 1 ATGGCGTCAA             Db 1 ATGGCGTCAA	Qy 61 GAGAGGGCTT             61 GAGAGGGCCTT	Qy 121 GCTGTCGGAG           Db 121 GCTGTCGGAG	Oy 181 CTCATCAACA             Db 181 CTCATCAACA	Oy 241 TCAAGAAGCA: Db 241 TCAAGAAGCA:
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Query Match 31.7%;
Best Local Similarity 75.4%;
Matches 150; Conservative
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ORGANISM: Gossypium hirsutum
                                                                                            ORGANISM: Gossypium hirsutum
FEATURE:
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US-10-021-323-16167/c
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LENGTH: 543
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Publication No. US20040181830A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TILLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
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                           301 regarararrregaraarcarreragregarrrregagaaarrereraaaaagrrerrera 360
                                                                                                                                                                       Sequence 1, Application US/10512600
Publication No. US20050210546A1
GENERAL INFORMATION:
APPLICANT: AGRINOMICS, LLC
TITLE OF INVENTION: GENERALION OF PLANTS WITH IMPROVED PATHOGEN RESISTANCE
FILE REFERENCE: AG03-033C-US
CURRENT APPLICATION NUMBER: US/10/512,600
CURRENT FILING DATE: 2002-104-10-22
PRIOR FILING DATE: 2002-104-10-22
PRIOR FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.2
SEQ ID NO 3.2
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100.0%; Pred. No. 2.8e-94;
tive 0; Mismatches 0;
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                                                                  AGTIATATITCTTIGGTTTAA 381
                                                                                                361 AGTTATATTTCTTTGGTTTAA 381
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; ORGANISM: Arabidopsis thaliana
US-10-512-600-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 381; Conservative
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Sequence 16167, Application US/10021323
; Sequence 16167, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
    APPLICANT: Peng, Paul C.C.
    APPLICANT: Fincher, Karen L.
    APPLICANT: Fincher, Karen L.
    APPLICANT: APPLICANTON: Plants
    TITLE OF INVENTION: Plants
    TITLE OF INVENTION: Plants
    FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 CATGGACGTTTAGTCAAAACAAGATGTTCGAGAGGGCCTTGGCAGTTTACGACAAGGACA
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                                                                                                                                                                                                                                                                                                                                                                                                  49; Indels
                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C42883_2
US-10-767-795-270
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US-10-021-323-16167
                                                                                                                                                                                                                                                                                                                                          Score 120.6; DB 8
Pred. No. 1.5e-22;
0; Mismatches 49
FILE REFERENCE: 38-21(53534)B
CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 117596
SEQ ID NO 270
LENGTH: 760
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APPLICANT: Zhou, Yihuas APPLICANT: Zhou, Yihuas APPLICANT: Kowalic, David K. APPLICANT: Kowalic, David K. APPLICANT: Kowalic, David K. APPLICANT: Screen, Steven E APPLICANT: Tabaska, Jack E APPLICANT: Tabaska, Jack E TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILLING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 14832 LENGTH: 704
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                                                                                                                               238 rictgaciccrcriscaccaaaacacaaacaacrcririgaaaaacacriscaaara 297
                                                                                                                                                                                 81 CGACAAGGACACCCCGACCGATGGCCACAATGTGGCAAAAGCTGTCGGAGGGAAAACTGT 140
                                                                                                                                                                                                                                 298 TGACAAGGATACCCCTGAGGCGCTGGCAGAATGTAGCCAAAGCAGTAGGTGGAAAATCTGC 357
                                                                                                                                                                                                                                                                                                                358 AGATGAAGTTAAGAGACACTATGAAATCCTCTTGGAGGATCTCAGACACATAGAGTCTGG 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   270 GCTGTTGGCAAAACTCCAGAGGAAGTGAAAAGGCACTACGAACTCCTTGTTCAGGAT 329
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                                                                               21 TTCAATCTCACCATGGACGTTTAGTCAAAACAAGATGTTCGAGAGGGCCCTTGGCAGTTTA
                                                                                                                                                                                                                                                                                   141 AGAAGAAGTGAAGCGCCACTATGACATTCTCGTCGAGGATCTCATCAACATCGAGACTGG
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                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 110.8; DB 7;
Pred. No. 7.3e-20;
0; Mismatches 72;
       Pred. No. 1.6e-21;
0; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: LIB3028-039-A6_FLI
US-10-425-114-14832
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; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14832, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
Best Local Similarity 70.1%;
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 29.1%;
Best Local Similarity 68.1%;
Matches 154; Conservative (
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ORGANISM: Glycine max
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US-10-424-599-135729
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US-10-424-599-6644

Sequence 6644, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION.

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Zhou Yihua

TITLE OF INVENTION: Plantes and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plantes and Uses Thereof for Plant Improvement

FILE REPERENCE: 38-21(5323)8

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT PLING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

FEAST
                                                                                                                                                                                            Sequence 271, Application US/10767795
Publication No. US20040181830A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT FILING DATE: 2004-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCGCCACTATGACATTCTCGAGGATCTCATCAACATCGAGACTGGTCGTGTCCCTT 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 AGAAGCACTATGAGCTTCTTCAAGATGTTAGACGCATCGAGTCGGGTCGGGTTCCTT 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 31.2%; Score 119; DB 8; Length 779; Best Local Similarity 74.9%; Pred. No. 4.3e-22; Matches 149; Conservative 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:

OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C42883_1
US-10-767-795-271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_106008C.1
US-10-424-599-6644
                                                                    325 rccccacrarredaccer 307
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                       TGCCCAATTACAAGACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Gossypium hirsutum
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LENGTH: 779
                       212
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Sequence 13836, Application US/10021323

Sequence 13836, Application US/10021323

Publication No. US20040123340A1

GENERAL INFORMATION:
APPLICANT: DelKman, Jill
APPLICANT: Feng, Faul C.C.
APPLICANT: APPLICANT: Alegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: NUMBER: US/10/021,323
CURRENT APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 13836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 CTTGGCAGTTTACGACAAGGACACCCCGACCGATGGCACAATGTGGCAAAAGCTGTCGG 128
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                                       209 AGAGAAAACTGTTGAGGAAGTGAAGAAGCACTATGAGCTTCTTCTTGAAGATGTTAGACG 268
                                                                                                       85 AAGGACACACCCGACCGATGCCACAATGTGGCAAAAGCTGTCGGAGGGAAAACTGTAGAA 144
                                                                                                                                                    347 AAGGACACGCCGACCGCTGGCACAACGTGGCGCGCGCCGCCGCGGCAAGTCAGCGGAA 288
                                                                                                                                                                                                         145 GAAGTGAAGCGCCACTATGACATTCTCGTCGAGGATCTCATCAACATCGAGACTGGTCGT 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

28.5%; Score 108.4; DB 7; Length
Best Local Similarity 68.0%; Pred. No. 3e-19;
Matches 151; Conservative 0; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 CATCGAGTCGGGTTCCTTTCCCCGACTATTGGACGT 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: LIB3829-015-Q1-K6-E2
US-10-021-323-13836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feng, Paul C.C.
Fincher, Karen L.
Ziegler, Todd E.
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APPLICANT: Feng, Paul C.
APPLICANT: Fincher, Kare
APPLICANT: Ziegler, Todo
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APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
EBQ ID NO 135729
LENGTH: 730
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APPLICANT: GOEFLY, Stephen A.
APPLICANT: GOEF, Stephen A.
APPLICANT: Katagiri, Fumiyaki
APPLICANT: Katagiri, Fumiyaki
APPLICANT: Kreps, Joel
APPLICANT: Ricke, Darrell
APPLICANT: Provart, Nicholas
APPLICANT: Zhu, Tong
TITLE OP INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR PELICATION NUMBER: US 60/325,448
PRIOR PELICATION NUMBER: US 60/325,277
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-26
NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
NUMBER: OS 5001-09-04
NUMBER: OS 5001-04-04
NUMBER: OS 5001-04-04
NUMBER: OS 50077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 28.9%; Score 110; DB 7; Length 466; Best Local Similarity 67.4%; Pred. No. 9.7e-20; Matches 155; Conservative 0; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 CTCATCAACATCGAGACTGGTCGTGTCCCTTTGCCCAATTACAAGA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                        Query Match 29.1%; Score 110.8; DB 7; Best Local Similarity 68.1%; Pred. No. 7.4e-20; Matches 154; Conservative 0; Mismatches 72;
                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT3847_93572C.1
US-10-424-599-135729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4786, Application US/10260238
Publication No. US20040016025A1
GENERAL INFORMATION:
APPLICANT: Budworth, Paul R.
APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
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LENGTH: 466
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APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERBNCE: 38-21(52274)B
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 115513.7 Application US/10021323
Publication No. US20040123340A1
GENERAL INFORMATION:
APPLICANT: Fend, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Fincher, Karen L.
APPLICANT: APPLICANT: Application Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR FILING DATE: 2000-12-14
PRIOR FILING DATE: 2000-12-14
                                      142 GAAGAAGTGAAGCGCCACTATGACATTCTCGTCGAGGATCTCATCAACATCGAGACTGGT 201
                                                                                             176 GAGGAAGTGAAGTTGCATTACCAGAACCTTGTGGATGACATCAAGCAGATAGAGTCTGGG 235
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US-10-021-323-11476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
28.2%; Score 107.4; DB 7;
Best Local Similarity 70.2%; Pred. No. 5.4e-19;
Matches 144; Conservative 0; Mismatches 61;
                                                                                                                                                                                                236 caccidectiricecectracades 260
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                                                                                                                                                                                                                                                                                                                              Sequence 11476, Application US/10021323 Publication No. US20040123340A1 GENERAL INFORMATION: APPLICANT: Deikman, Jill
                                                                                                                                              202 CGTGTCCCTTTGCCCAATTACAAGA
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SEQ ID NO 11476
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US-10-021-323-11476
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (52274)B
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 16005
LENGTH: 505
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APPLICANT: Fincher, Karen L.
APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: NUCLEIC Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(52274)B
CURRENT EPPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
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Pred. No. 5.3e-19;
0; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: LIB3829-034-Q1-N6-A10 US-10-021-323-16005
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; OTHER INFORMATION: Clone ID: LIB3829-034-Q1-K6-Al0
US-10-021-323-14482
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Publication No. US20040123340A1
GENERAL INFORMATION:
APPLICANT: Deikman, Jill
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 70.2%;
Matches 144; Conservative
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ORGANISM: Gossypium hirsutum
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US-10-021-323-14482
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LENGTH: 532
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US-10-767-795-5000

Sequence 5000, Application US/10767795

Sequence 5000, Application US/10767795

Sequence 5000, Application US/10767795

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REPERENCE: 38-21(53534) B

CURRENT FILING DATE: 2004-01-30

NUMBER OF SEQ ID NOS: 117596

SEQ ID NO 5000

LENGTH: 604
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Pred. No. 5.8e-19;
0; Mismatches 61; Indels 0
                                                                                                                                                 Length 542;
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; OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C53491_1
US-10-767-795-5000
                                                                                      ; OTHER INFORMATION: Clone ID: LIB3829-002-Q1-N6-E10
US-10-021-323-11563
                                                                                                                                              Query Match 28.2%; Score 107.4; DB 7; Best Local Similarity 70.2%; Pred. No. 5.5e-19; Matches 144; Conservative 0; Mismatches 61;
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Best Local Similarity 70.2%;
Matches 144; Conservative 0
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ORGANISM: Gossypium hirsutum
                                  TYPE: DNA ORGANISM: Gossypium hirsutum
SEQ ID NO 11563
LENGTH: 542
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Seguence:

Scoring table:

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AC157502 Medicago
AK112054 Oryza sat
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AL01589 Arabidopsis
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AP007251 Oryza sat
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AP004317 Oryza sat
AP004317 Oryza sat
AC06439 Arabidops
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AC07301 Lotus Cor
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Continuation (287
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AY519531 Arabidops
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AK118891 Arabidops
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KTVEEVKRHYDILVEDLINIETGRVPLPNYKTFESNSRSINDFDTRYITKYLYMMLSI
YFDNHSSDFEKFSQKVLVSYISLV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (Dases 1 to 381)

Qu. L. and Gu.H.

The MYB Transcription Factor Family in Arabidopsis: A Genome-Wide Cloning and Expression Pattern Analysis
Unpublished
Unpublished
Unpublished
Unpublished
Univ. and Gu.H.

Direct Submission
Submitted (07-JAN-2004) Life Sciences, National Laboratory of Protein Engineering and Plant Genetic Engineering, Peking University, Beljing 100871, China
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="MYB transcription factor"
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/organism="Arabidopsis thaliana"
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AC120988
AC162787
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AP007301
AC146974
AC007858
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AK112054
ATAP22
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AP008207_:
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CS137908
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27.1 108844
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BT005657 Arabidops
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AJ277944 Lycopersi
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AP008039 Locus cor
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CS138004 Sequence
                                                                                    March 10, 2006, 18:29:10 ; Search time 2275 Seconds (without alignments) 9519.716 Million cell updates/sec
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                                                                                                                                                                                                                                                                 11766282
           GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                    5883141 segs, 28421725653 residues
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Maximum Match 100%
Listing first 45 summaries
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AK119034
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AJ583670
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9b_on:**
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clone.

Genes were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, http://CRC.081.mtt.ed/GENSCAN.html), GeneMarkHMM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMarkHMM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant of GlimmerM, see Mihaela Pertea, http://www.tigr.org/offlab/glimmerm.htm/glimmerm.html, and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein prodeins over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.washington.edu/RM/Repeatmasker.html).
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GEEGEESCRSSMEEGGDATSDIGAATDGNMKENGEESCRSSMEEGGDATSDISONKA
FTYGEHLKKT DETREKEREKOENVWPRAIFEAFRAFADAMERAGKTAMEKAKAVA
HTREVPRKGEKGSVENDKLSSAEKASMQAKLRAERAAVERAITEVBERAMEKALSGK
SAASQAKSYGGSKSFSSGERRGSSSGGTENKSSGPSNSSNQTGEPIORCKARSERHQ
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                                                                                                                                                          BAC clone F22H5 is from Arabidopsis thaliana chromosome 1 The orientation of the sequence is from SP6 to T7 end of the BAC
                      Town,C.D. PhD.
Direct Submission
Submitted XAN-2001)
On Jan 22, 2001 this sequence version replaced gi:12280794.
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Address all correspondence to:at@tigr.org
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complement(418..5404)
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(bases 1 to 68041)
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Arabidopsis thaliana (winate Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Viridiplantae; Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, eudicotyledons; core eudicotyledons; rostids; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

1. (bases 1 to 68041)

Lin,X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B.J., Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujia,C.Y., Utterback,T.R., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M. Arabidopsis thaliana chromosome 1 BAC F22H5 genomic sequence
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Arabidopsis thaliana chromosome 1 BAC F22H5 genomic sequence,
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Direct Submission
Submistred (12-oct-2000) The Institute for Genomic Research, 9712
Submitted (12-oct-2000) The Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org
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                                                                                                                       1 ATGGCGTCAAACTCCAAGAAGTTCAATCTCACCATGGACGTTTAGTCAAAACAAGATGTTC
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Trown,C.D. and Kaul,S.
Direct Submission
Submitted (05-007-2000) The Institute for Genomic Research, 9 Medical Center Dr. Rockville, MD 20850, USA, cdtcom@tigr.org 5 (bases 1 to 68041)
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                           Length 381;
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                        100.0%; Score 381; DB 15;
100.0%; Pred. No. 3.4e-84;
ive 0; Mismatches 0;
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LEVALGHYKOWSVPESLITSVRNYAKALFSRESFENTKAKKEIVVAGWESKVNA"
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGGCGTCAAAACTCAAGAAGTTCAATCTCACCATGGACGTTTAGTCAAAACAAGATGTTC
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/gene="F22H5.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 68041;
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Pred. No. 3.4e-84;
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Patent: WO 2005047316-A 975 26 MAY-2005;
Mendel Blotechnology, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CS138004 294 bp DNA Sequence 975 from Patent WO2005047516.
                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Scor...
100.0%; Pred. No. J...
7. 0; Mismatches
                                                                                                                                                 complement (16410. .18554)
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CS138004.1 GI:72058666
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                                                                                                                                                                                                                                                                                                                                /product="NADPH oxidoreductase, putative; 10572-9197"
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LRTLQPESGLISHTRDKAIIFEDKOVIPOKVTIGDGNAKVVINKEEDVAAYMIKA
VDDLRTLNKTISPPRNILSMNEMYTWEKKIGKSLEKTHISEEQILKSIQVPIDVF
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VCKGDQTNFTIEBSFGFRASELYPDIKYTSIDEYLSYFALGTSLNT"
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/note="mainiar to GI:6939839 from [Oryza sativa]"

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                                                                       gene
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Arabidopsis thaliana (mars Cross)

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae, Arabidopsis.

I (bases 1 to 334)

Standa, K., Chan, M., Chang, C.H., Dale, J.M., Heuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Reker, J.R. and Theologis, A.

Arabidopsis Open Reading Frame (ORF) Clones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BT005657 334 bp mRNA linear PLN 15-MAR-2003
Arabidopsis thaliana clone U51233 putative myb family transcription
factor (At1g19510) mRNA, complete cds.
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The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yuan, S., Carninoi, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Suturai, T., Shinozaki, K., Davis, R.W., Direct Submission
                                                                                                                                    GAGAGGCTTTAGCCGTTTACGATAAAGACACTCCCGACCGTTGGCAAACGTGGCTAAA 120
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                                                                                          181 crcargaacarcaagacrragraccrricccraaraccaaacccraccaaacccaaccarcaaccaacca
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                                                                                                                                                                                               121 GCTGTCGGAGGGAAAACTGTAGAAGAAGTGAAGCGCCACTATGACATTCTCGTCGAGGAT
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ATGGCGTCAAACTCAAGAAGTTCAATCTCACCATGGACGTTTAGTCAAAACAAGATGTTC
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Arabidopsis thaliana (thale cress)
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                                                                                                                                                                                                     1 ATGGCGTCAAACTCAAGAAGTTCAATCTCACCATGGACGTTTAGTCAAAACAAGATGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 bp mRNA linear PLN 07-FEB-
transcription factor (At1g19510) mRNA,
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Submitted (07-JAN-2004) Life Sciences, National Laboratory
Protein Engineering and Plant Genetic Engineering, Peking
University, Beijing 100871, China
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                                                                        Length 294;
                                                                                                                         Indels
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0; Mismatches 6
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Arabidopsis thaliana
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Arabidopsis thaliana MYB
complete cds.
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                                                                           71.8%;
97.9%;
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Qu, L. and Gu, H.
                                                                                                  Local Similarity 97.9
hes 277; Conservative
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Matches 210;
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                                                                             Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AK119034 14-FEB-2004 Arabidopsis thaliana At1g19510 mRNA for putative myb-related protein, complete cds, clone: RAFL21-36-F10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GAGAGGGCTTTTAGCCGTTTACGATAAAGACACTCCCGACCGTTGGCAAAACGTGGCTAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGTCGGAGGGAAAACTGTAGAAGAAGTGAAGCGCCACTATGACATTCTCGTCGAGGAT 180
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Annotation based on July 2002 version of the Arabidopsis genome
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Arabidopsis thaliama full-length cDNA
Published Only in Database (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 580)
Seki,M., Iida,K., Satou,M., Sakurai,T., Akiyama,K., Ishida,J.,
Nakajima,M., Enju,A., Kamiya,A., Narusaka,M., Carninci,P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 39.7%; Score 151.4; DB 15; Length 334; Best Local Similarity 73.2%; Pred. No. 5.5e-27; Matches 210; Conservative 0; Mismatches 71; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 TCTAACTCAAGAAGCATCAATGACTTTGACACAAGGTATATAACTAA
                                                                                                                                                                               /ecotype="Columbia"
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                                                                               thaliana"
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AK119034
AK119034.1 GT:26453067
AK12 CDNA; CAP trapper.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           304. .334
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                                                                                                                                                                                                                                                          .303
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Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 GAGAGGCTTTAGCCGTTTACGATAAAGACACTCCCGACCGTTGGCAAAACGTGGCTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="common name: thale cress"
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Best Local Similarity 73.2%; Pred. No. 5.5e-27;
Matches 210; Conservative 0; Mismatches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="At1g19510/F18014_31"
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1. .580
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AC025808.8 GI:7636235
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join(17994. 18489,18568. 18698,18814. 18847,19006. 19099,
19170. 19347,19441. 19479,19616. 19715,19855. 19994)
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KVDLSKLEMPALLNYWRHFNLVDAIPNPSKEQLIDIVQRHFMSQQMDELQVIVGFVQA
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ALKGI I PNI VTYNALI KGLCKLGNVDRAQRLLHKLPQKGI TPNA I TYNTLI DGLVKSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SASADASSLRATISSSFPYLDFTVYVFNVSSVSRLISSSIRSALDCPLNYARSYLADL
LPPCVRRVVYLDSDLILVDDIAKLAATDLGRDSVLAAPEYCNANFTSYFTSTFWSNPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="WSDVPSGSSGNDTNNNDSSNFECNICLDLAQDPIVTLCGHLFCW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MAIFSTSHLLFISFIIATCTISVSGTTFTLTNHCGSTIWPGILTANGAQLGDGGFALASGSSVTFTVSPGWSGRFWARTYCNFDASGSGKCGTGDCGSKLKCAGAGGAPPATLAEFTIGSSGKKNAVQDFYDVSLVDGYNVQMKITPQGGSGDCKTAGCVSDVNAICPKELQVTGPSGVAACKSAGEAFNKPEYCCTGAYSTPATCPFTNYSKIFKQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CPSAYSYAYDDASSTFTCTNANYEISFCS"
complement (join(14020, .14136,14236, .14304,14402, .14464,
14557, .14696,14879, .15005,16274, .16486))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GFPDAAMYGAAASGGFPHGFSNPFHGGHSHMHSYQRHTGRQGQDHHLRILLLIVFVV
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/note="unknown protein; similar to ESTs gb|A1992723.1,
                                                                                                                            note="putative glycosyltransferase-like protein
emb|CAB42905.1; similar to EST gb|A1998490.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (9620. .10300)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(12523. .12577,12686. .13374)
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                                                                                                                                                                                                                                /evidence=not_experimental/product="F18014.2"
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                                                                                                .5702)
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                                                                                                complement (4647.
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Direct Submission

L. Submitted (22-APR-2000) Arabidopsis thaliana Genome Center,

Submitted (22-APR-2000) Arabidopsis thaliana Genome Center,

Department of Biology, University of Pennsylvania, 38th Street and

Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA

18 (bases 1 to 120977)

Cheuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, O.,

Choo, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N.,

Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N.,

Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H.,

Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M.,

Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chao, Q., Brooks, S., Buehler, B., Johnson-Hopson, C., Khan, S., Kim, C., Shinn, P., Altafi, H., Bei, B., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Hwwing, B., Koo, T., Lam, B., Nguyen, M., Palm, C., Liu, A., Liu, J., Liu, S., Mukharsky, N., Thaveri, M., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J. G., Davis, R., Direct Submission
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                           Shinn, P., Brooks, S., Buehler, E., Chao, Q., Johnson-Hopson, C., Shinn, P., Kim, C., Altafi, H., Bei, Q., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzales, A., Hansen, M., Howing, B., Koo, T., Lam, B., Lee, J., Lee, J., Lee, J., Liu, A., Liu, R., Liu, S., Mukharsky, M., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Federspiel, N. A., Theologis, A. and Ecker, J. R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (15-MAR-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (bases 1 to 120977)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (28-UNN-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA 5 (bases 1 to 120977)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (11-OCT-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA On Apr 22, 2000 this sequence version replaced gi:7543634.
   eurosids II; Brassicales; Brassicaceae; Arabidopsis
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Corganism="Arabidopsis thaliana"
/mol type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                      Unpublished
2 (bases 1 to 120977)
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                                                                                                                                                                                                                                                                                                                                           chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AJS83670 36-JAN-2004 JAN linear PLN 30-JAN-2004 Lycopersicon esculentum faml gene for SANT/MYB protein, exons 1-2.
                                                                    AJ277944.1 GI:7981379
famil gene; SANT/MTB domain protein.
Lycopersicon esculentum
Lycopersicon esculentum
Lycopersicon esculentum
Estraryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
                                                                                                                                                                                                                                                         Sobolev,I., Chmelnitsky,I., Barg,R. and Salts,Y. The tomato early fruit specific gene LeFSM1 defines a novel class of plant-specific SANT/MYB domain proteins unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 ACGACAAGGACACACCCGACCGATGGCACAATGTGGCAAAAGCTGTCGGAGGGAAAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 ATGACAAGGAAACTCGCGATCGTTGGTCCAATGTTGCTAAAGCAGTTGGAGGCAAAACAG
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    Lycopersicon esculentum mRNA for SANT/MYB domain protein (fsml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 GITCAAICTCACCAIGGACGITIAGICAAAACAAGAIGIICGAGAGGGCCTIGGCAGITI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Lycopersicon esculentum"
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/du type="fruit"
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1. .61.
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                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (12-MAY-2000) Salts Y., Plant Genetics,
Center, ARO, PO Box 6, Bet-Dagan, 50250, ISRAEL
Location/Qualifiers
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AJS83670.1 GI:36783451
Ball gene; SANT/MYB protein.
Lycopersicon esculentum (Solanum lycopersicum)
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/gene="fsml"
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Salts, Y.
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AJ277944.1
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                                           ACCESSION
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    DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90486 ATGGCCTCTAGTTCTATGAGCTCGAGCTCTTTGGACGTCTAAGCAAAACAAGATGTTC 90427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90426 GAGAGGGCTTTAGCCGTTTACGATAAAGACACTCCCGACCGTTGGCAAAACGTGGCTAAA 90367
                                                                                                                                                                               KIYTGLRAQCNYNLPKHCDNNEVLKALCSEAGWVVEEDCTTYRKGHKPLPGDMAGSSS
RATPYSSHNQSPLSSTFDSPILSYQVSPSSSSFPSFSRVGDPHNISTIPPFLRNGGIP
                                                                                                                                                                                                                              SSLPPLRISNSAPVTPPVSSPTSRNPKPLPTNESFTKOSMSMAKOSMTSLNYPFYAV
SAPASPTHHROFHAPATIPECDESDSSTVDSGHWISFOKFAQQQPFSASMVPTSPTFN
LVKPAPQQLSPNTAAIQEIGQSSEFKFENSQVKPWEGERIHDVAMEDLELTLGNGKAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALANANYKAMLEVOTASTKRVOTTNYLVVALDDYTENICKENDVAYYKRDPDKDVDTV
GKTGGNHAVSGLKFRVLREFLQLGYGYLLSDVDTVFLQNPFSHLYRDSDVESMSDGHD
NHTAYGFNDVFDEPAMGWARYAHTWRTWVFNSGFFYLRPTTPSTELDRVADRLSKAK
VWDQAVFNBELFYPSHPEYTALHASKRVMDMYEFMNSKVLFKTVRKNHELKKKVKPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tränblation="MADPLNGKSFFICFSLLFSFTLLFISPLYATESPVIEDVSTDVA
VSVSSTNREAVLLHNLEELVKNLTELVANLDAKLSAPPLKEKNBISVDDDIGBEKERG
VRARFSVYKTSPFWSERFQFTSAVKLNSDATCINVLPFRDFEGSKYYFAIGDSKRVY
VFLRNGDVLIEFFTTVDSPVTAMVSYSVFKNSFVTGHQNGAVLLHRIHGGSNGED
WNSNSVSMEHYGKFDVDDSADPYTLLEVHHVGRVRYILLATDLGGKLTVLTENRTVYGS
VIPSSRPLVFLKQRLLFLTESGAGSLDLRSMKIRETECEGLNHSLARTYVFDAAERSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="magrrdrsqqlrgsrialailigipigcycavlppygffnssss
Lkasehlskssnovgssacespervkmlksdfytlseknaelkkgyrelteklrlaeg
Gsdnarkgyllalgtqikagppgtvkslrtnptilpdesinprlakileelavdkeviv
                                                                                                                                                              translation="MTSDGATSTSAAAAAAAAATRRKPSWRERENNRRERRRRAVAA/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLN 03-FEB-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GCTGTCGGAGGGAAAACTGTAGAAGAGAGTGAAGCGCCACTATGACATTCTCGTCGAGGAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCATCAACATCGAGACTGGTCGTGTCCCTTTGCCCAATTACAAGACCTTCGA-----A 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VHVNYHPDKLNRMQAVVEFYVNGKQDALDSFPDGSE"
complement (26100. .27917)
/nocte="unknown protein; similar to ESTs gb|T42717.1,
emb|P13886.1, and emb|F13885.1"
                                                                                                                                                                                                                                                                                                                           complement(join(23868. .24983,25237. .25407))
//note="unknown protein; similar to EST gb|T13858.1,
emb|238050.1, and emb|238087.1"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 120977;
T41777.1, dbj AV440980.1, gb AI997341.1, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 149.4; DB 1
Pred. No. 1.7e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental
/product="F18014.8"
/protein_id="AAF79453.1"
/db_xref="G1:8778445"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                 /evidence=not_experimental
/product="F18014.7"
/protein_id="AAF79422.1"
/db_xref="G1:8778414"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
/product="F18014.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAF79452.1"
/db_xref="G1:8778444"
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Best Local Similarity 74.0%;
Matches 205; Conservative
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LES277944
LOCUS
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                                                                                      PLN 14-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                Submitted (14-JAN-2004) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                              Eukaryota, Viridiplantae, Straptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GCTGTCGGAGGGAAAACTGTAGAAGAAGTGAAGCGCCACTATGACATTCTCGTCGAGGAT 180
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                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 246)
Cheuk, R., Chen, H., Kim, C.J., Shinn, P. and Ecker, J.R.
Direct Submission
                                                                                                                                                                                                                                                                    1 (bases 1 to 246)
Cheuk, R., Chen, H., Kim, C.J., Shinn, P. and Ecker, J.R.
Arabidopsis ORF clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BT010770 506 bp mRNA linear Arabidopsis thaliana At4936570 mRNA, complete cds. BT010770 GI:38566493 FLI_CDNA.
                                                                                    BT011255 246 bp mRNA linear Arabidopsis thaliana At4g36570 gene, complete cds. BT011255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .246
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 2.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /ecotype="Columbia"
/note="This clone is in pUNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 28.5%; Score 108.4; Best Local Similarity 68.0%; Pred. No. 2.86 Matches 151; Conservative 0; Mismatches
2711 GTATGGTGCCCTTCCCCAAATACAAAC 2738
                                                                                                                                                           FLI CDNA.
Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="C62918"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome="4"
                                                                                                                                          BT011255.1 GI:40823587
                                                                                                                                                                                                Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                        Unpublished
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LOCUS
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                                                    RESULT 10
BT011255
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                                                                                                                                            VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MSSMSSQHGSSGSWTAKQNKAFEKALAVYDKETRDRWSNVAKAV
GGKTAEEVKRHYEILLRDVFFIDNGMVPFPKYKTTGGSHNSTSD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2531 GITCTTCTGGATCATGGACTGCGAACAAAGAGGCGTTTGAGAAGGCATTGGCTGTGT 2590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2591 ATGACAAGGAAACTCGCGATCGTTGGTCCAATGTTGCTAAAGCAGTTGGAGGCAAAACAG 2650
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              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
                                                                                      Sobolev, I., Chmelnitsky, I., Barg, R. and Salts, Y.
The tomato early fruit specific gene LeFSM1 defines a novel class of plant-specific SANT/MYB domain proteinsl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 GITCAATCICACCATGGACGITTAGICAAAACAAGAIGITCGAGAGGGCCTIGGCAGITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 ACGACAAGGACACACCCGACCGATGGCACTATGTGGCAAAAGCTGTCGGAGGGAAAACTG
                                                                                                                                                           Chases I to 3605)
Salts, Y.
Direct Submission
Submitted (25-SEP-2003) Salts Y., Plant Genetics, The Volcani
Center, ARO, PO Box 6, Bet-Dagan, 50250, ISRAEL
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                              . .930
transposon="retrotransposon like sequence"
                                                                                                                                                                                                                                                                                                                                                                                                 1232. 1523
| Kransposon="foldback transposon TAPIR1"
2385. 3605
| Gene="fsm1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                   /organism="Lycopersicon esculentum"
/mol_type="genomic DNA"
/db_xref="taxon:4081"
/chromosome="10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 108.8; DB 15;
Pred. No. 2.2e-16;
); Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .3605)
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product="SANT/MYB_protein"
protein_id="CAE47523.1"
db_xref="GI:36783452"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 GTCGTGTCCCTTTGCCCAATTACAAGAC 227
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gene≂"fem1"
420
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/gene="fem1"
join(2429. .2
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ilarity 70.2%;
Conservative 0
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gene="fsm1"
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/gene="fsml"
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Submitted (26-001-2004) Shusei Sato, Kazusa DNA Research Institute, Department of Plant Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu, Chiba, 292-0818, Japan (E-mail:ssato@kazusa.or.jp, UKL:http://www.kazusa.or.jp/, Tel:81-438-52-3935(ex.2337), Fax:81-438-52-3934)

* NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
Features and Mapping of Nine hundred twenty-one TAC Clones Unpublished
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/clone="LjT05D15"
/clone lib="LjT library"
/ncte="Thota" clone:TM1490, synonym:Lotus japonicus"
5203. 5302
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gap of unknown length
contig of 8837 bp in length
gap of unknown length
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gap of unknown length
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gap of unknown 1
contig of 5704 b
gap of unknown 1
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3625. .8724
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variety="japonicus"
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                                            (bases 1 to 100108)
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                                                                Sato, S.
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                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="At4g36570"
/protein id="AAR24137.1"
/bxref="G1:3856494"
/translation="WASNSMSSSASWTRKENKLFERALATYDQDTPDRWHNVARAVGG
KSAEEVRRHYELLIRDVNDIESGRYPHPNYRSNGNNH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AP008111 100108 bp DNA linear HTG 28-DEC-2004
Lotus corniculatus var. japonicus clone LjT05D15, *** SEQUENCING IN
PROCESS ***, 20 unordered pieces.
                                                                                                                                    Unpublished
Unbublished
2 (base 1 to 506)
Cheuk, R., Chen, H., Kim, C.J., Shinn, P. and Ecker, J.R.
Direct Submission
Submitted (29-NOV-2003) Salk Institute Genomic Analysis Laboratory (SIGnAL), Plant Biology Laboratory, The Salk Institute for Usal Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
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                    Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosida II, Brassicales, Brassicaceae, Arabidopsis.
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Lotus corniculatus var. japonicus
Eukaryota, Viridiplantae; Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GAGAGGCCTTGGCAGTTTACGACAAGGACACCCGACCGATGGCACAATGTGGCAAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 GAAAGGGCGTTGGCTACATATGACCAGGACACTCCTGACCGTTGGCATAACGTTGCAAGA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGTCGGAGGGAAAACTGTAGAAGAAGTGAAGCGCCCACTATGACATTCTCGTCGAGGAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 ATGGCTTCCAACTCAATGAGCTCTTAGCGCTTCTTGGACACGTAAGGAGAACAAATTATTT 93
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Structural Analysis of a Lotus japonicus Genome. XI. Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.5%; Score 108.4; DB 15; Length 506; 68.0%; Pred. No. 2.8e-16; ive 0; Mismatches 71; Indels 0;
                                                                                        1 (bases 1 to 506)
Cheuk, R., Chen, H., Kim, C.J., Shinn, P. and Ecker, J.R. Arabidopsis cDNA clones
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/organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51,
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/note="This clone is in pUNI
    Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="unknown protein"
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                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                              'clone="S62918"
                                                                                                                                                                                                                                                                                                                                                                                                          chromosome="4"
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HTG; HTGS PHASE1.
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VERSION
KEYWORDS
SOURCE
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                                                                                                           5.4 Mb
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Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus
Liotus corniculatus var. japonicus
Eukaryota; Viridiplantas; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                      Sato,S., Kaneko,T., Nakamura,Y., Asamizu,E., Kato,T. and Tabata,S. Structural Analysis of a Lotus japonicus Genome. I. Sequence Features and Mapping of Fifty-six TAC clones which cover the 5.4 M Regions of the Genome
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                   Direct Submission
Submitted (13-DEC-2001) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
URL:http://www.kazusa.or.jp, Tel:81-438-52-3935,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 97268;
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                                                                                                                                                                                                                                                                                                                                  /organism="Lotus corniculatus var. japonicus"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
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/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 106.6; DB 15; Length
Pred. No. 7.9e-16;
0; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synonym: Lotus japonicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="LjT_library"
/note="TAC_clone:TM0178
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Location/Qualifiers
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                                                                                                                                Regions of the Genome
Unpublished
2 (bases 1 to 97268)
Nakamura, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 28.0%;
Best Local Similarity 70.6%;
Matches 142; Conservative
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Direct Submission
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AP008039/c
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Lotus corniculatus var. japonicus
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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58.5%; Pred. No. 2.8e-16;
ive 0; Mismatches 146;
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/estimated_length-unknown
13796. 13895
/estimated_length-unknown
15743. 15842
/estimated_length-unknown
19032. 19131
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36586. 38685
/estimated_length=unknown
42390. .42489
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21811. .21910
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24668. .24767
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AP004546/c
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/ estimated_length=unknown 55925691	/ 7119 17218    17119 17218   17119 17218   18119 17218   18119 17218   18119 17218   18119 17218   18119 18119   18119 1819   18119 18119   18119 18119   18119 18119   18119 18119   18119 18119   18119 18119   18119 18119   18119	Query Match         28.0%;         Score 106.6;         DB 14;         Length 102550;           Best Local Similarity 70.6%;         Pred. No. 7.98-16;         Antels 0;         Gaps 0;           Matches 142;         Conservative 0;         Mismatches 59;         Indels 0;         Gaps 0;           Qy         28 TCACCATGGACGTTACAAACAGACTCTCGAGAGGCCTTACGACAAG 87         B         GACACACCCGACGATGGCAAACTGTCTTCGAGAGCACTTGCAAAATTACGACAG 96815           Qy         88 GACACACCCGACGATGGCAAAAGTTGTTCGAGAGCACTTGCAAAATTACGAGAGAAA 147
Gene Research; 2-6-7 I Gene Research; 2-6-7 I an (E-mail:ssato@kazus a.or.jp/, Tel:81-438-5 orking draft' sequence tigs. The true order their order in this settween the contigs are exact sizes of the ge e updated with the fire vallable and the acceptant	1 3089: contig of 3089 bp in 1 3089: and 9189: gap of unknown length 4483 4582: gap of unknown length 4483 5591: contig of 1089 bp in 1 5592 5691: contig of 1089 bp in 1 5592 5691: contig of 1089 bp in 1 5692 5691: contig of 1089 bp in 1 6881: gap of unknown length 8736: gap of unknown length 8737: gap of unknown length 10515: contig of 1577 bp in 1 10515: contig of 1577 bp in 1 11894 10513: contig of 1279 bp in 1 11894 10518: gap of unknown length 17718: contig of 2271 bp in 1 17119 1795: contig of 2577 bp in 1 17119 1795: gap of unknown length 17218: gap of unknown length 17218: gap of unknown length 17218: gap of unknown length 23149: gap of unknown length 23149: gap of unknown length 23149: gap of unknown length 25547: contig of 3189 bp in 1 25547: gap of unknown length 25547: gap of unknown length 25547: gap of unknown length 26557: gap of	41223: contig of 4110 41223: gap of unknows 46817: contig of 5494 56494: contig of 7577 56499: contig of 7577 56493: gap of unknows 64935: contig of 1034 65035: gap of unknows 74018: gap of unknows 88264: contig of 1414 88364: gap of unknows 100720: contig of 1237 10820: gap of unknows 100820: gap of unknows 10820: gap of unknows 102550: contig of 1237 102550: contig of 1237 102550: contig of 1238 102550: contig of 1238 100820: ganomic DNA ariety="japonicus" brome="Littlop24" 10ne="Littlop24" 1

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58455 GACACCCTGAGCGGTGGCAAAATGTGTCCAAAGCAGTTGGTGGCAAATCAGTGGAGGAA 58396
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                                                                                                                                                                                  /clone lib="LjB library"
/note="BAC clone:BM1105, synonym:Lotus japonicus"
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                                                                     /organism="Lotus corniculatus var. japonicus"
/mol_type="genomic DNA"
/varīety="japonicus"
5 93184: gap of unknown length
5 108878: contig of 15694 bp in length.
Location/Qualifiers
1. .108878
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llarity 70.6%; Pred. No. 7.9e-16;
Conservative 0; Mismatches 59;
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/estimated length=unknown
12080. .12179
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.49<u>9</u>95
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/estimated length=unknown 67741. .67840
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13220. .13319
/estimated_length=unknown
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20911. .21010
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23212. .23311
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19861. 129960
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39621. .39720
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15218. .45317
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5708. .6807
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                                                                                                                                                                  clone="LjB04J07"
                                                                                                                                                 chromosome="1
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Matches 142;
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                                                                                                                                                                                                                                                         Direct Submission

Submitted (26-OCT-2004) Shusei Sato, Kazusa DNA Research Institute,

Submitted (26-OCT-2004) Shusei Sato, Kazusa bNA Research Institute,

Chiba, 292-0818, Japan (B-mail:ssato@kazusa.or.jp,

Chiba, 292-0818, Japan (B-mail:ssato@kazusa.or.jp,

URL:http://www.kazusa.or.jp/, Tel:81-438-52-3935(ex.2337),

Fax:81-438-52-3934)

* NOTE: This is a "working draft' sequence. It currently

* Consists of 24 contigs. The true order of the pieces

* a not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                 Lotus cormiculatus var. japonicus (Lotus japonicus)
Lotus cormiculatus var. japonicus
Lotus corniculatus var. japonicus
Stratycus Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                               Kaneko,T., Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Structural Analysis of a Lotus japonicus Genome. XI. Sequence
Features and Mapping of Nine hundred twenty-one TAC Clones
Unpublished
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APPLICANT: Wood, Marion

APPLICANT: Shenk, Michael A.

APPLICANT: Glenn, Matthew

TITLE OF INVENTION: Compositions and Methods for the

TITLE OF INVENTION: Modification of Gene Transcription

FILE REFERENCE: 11000.1021C1U

CURRENT PELLING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 2368

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                        US-09-949-016-14033
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4979.787 Million cell updates/sec
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381
1 atggcgtcaaactcaagaag......gttatatttctttggtttaa
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                                GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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/cgn2_6/ptodata/1/ina/5_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PP_COMB.seq:*
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US-09-640-211A-1531
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US-09-649-016-17031
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US-09-949-016-13657
US-09-949-016-13657
US-09-949-016-14207
US-08-453-866-11
US-08-453-866-11
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US-08-454-097-9
US-09-949-016-15563
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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APPLICANT: Jobert, S. APPLICANT: Jobert, S. TILLE, CANT: Glordano, J.Y. TILLE PER PROPERTION: ESTS AND ENCOded Human Proteins. FILE REFERENCE: GRNSET.054PR2. CURRENT APPLICATION NUMBER: US/09/621,976. CURRENT FILING DATE: 2000-07-21. WUMBER OF EQ. ID NOS: 19335. SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
10.6%; Score 40.2; DB 3;
Best Local Similarity 60.6%; Pred. No. 0.57;
Matches 66; Conservative 0; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-09-621-976-8976/c
Sequence 8976, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LUCCATION: (1)...(100863); OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17031
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                                 372 TAAGCACTATCA 383
153 GCGCCACTATGA 164
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Matches 33; Conserv
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ORGANISM: Human
                                                                                                                     RESULT 4
US-09-949-016-17031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 GTCGGAGGGAAAACTGTAGAAGAAGTGAAGCGCCACTATGACATTCTCGTCGAGGATCTC 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                            15.3%; Score 58.4; DB 3; Length 357; 54.7%; Pred. No. 3.4e-07; ive 0; Mismatches 96; Indels
     APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Compositions of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ 1D NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ 1D NO 1581
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APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Glenn, Matthew
ITILE OF INVENTION: Compositions and Methods for the
ITILE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FASTSEQ for Windows Version 4.0
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Patent No. 6833446
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; ORGANISM: Eucalyptus grandis
US-09-640-211A-1310
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Matches 116, Conservative
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  GENERAL INFORMATION:
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LENGTH: 383
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                                                                                                                                                                                                                                                                                            43; Indels
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Sequence 14207, Application US/09949016

Sequence 14207, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 TACAAGACCTTCGAATCTAACTCAAGAAGCATCAATGACTTTGACACAAGGTATAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.8%; Score 37.4; DB 3; Length 670689; Best Local Similarity 53.0%; Pred. No. 7.8; Matches 80; Conservative 0; Mismatches 71; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 670690;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340 TICICICAAAAAGTICITGIAAGTIATATTI 370
                  CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-06
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PRESCR FOR WINDOWS VERSION 4.0
SSOFTWARE: FASELSOFT
                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (1)...(670689)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LUCATION: (1) ... (670690)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14207
         REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
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US-09-949-016-14207/c
                                                                                                                                                                                                                                                                                                          ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-949-016-12505
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                                                                                                                                                                                                                                                                                          TYPE: DNA
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                   229 TICGAAICTAACTCAAGAAGCAICAATGACTTTGACACAAGGTATATAACTAAATATCTA 288
277 RWSYRRAMWRGSKSWGGGSYYRMAGYRSSRWRSWYSAMWRKKKMTCWKGRSSWGSRSTGY 218
                                          AATGTGGCAAAAGCTGTCGGAGGAAAACTGTAGAAGAAGAGGGCGCCACTATGACATT 168
                                                                                                                              CTCGTCGAGGATCTCAACATCGAGACTGGTCGTGTCCCTTTGCCCAATTACAAGACC 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 ATCTATATATGATGCTCTCGATATATTTTGATAATCATTCTAGTGATTTTTGAGAAATTCT 343
                                                                                                                                                       157 YYYKSYMSMKKIWRMKTAYYWTKRWK-MTRTKWTWCTMCWKCTTYWMAGTWMYRYRRRYW 99
                                                                                                                                                                                                                                             98 YYAKRAKWSKRCTWSTTCYCMKYMAKKCWSYWWSMWKWGKSMWWKWTYYYYYYMMKWS 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224 AGACCTTCGAATCTAACTCAAGAAGCATCAATGACTTTGACACAAGGTATATAACTAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     344 CTCAAAAGTTCTTGTAAGTTATATTTCTTT 374
                                                                                                                                                                                                                                                                                                      289 TATATGATGCTCTCGATATATTTTGATAAT 318
                                                                                                                                                                                                                                                                                                                               KMTYWSMMSCYARKCWRTYAKTYTWMTCMT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 13667, Application US/09949016
; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12505, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: misc_feature
; LCCATION: (1)...(89892)
; OTHER INFORMATION: n = A,T,C or
US-09-949-016-13667
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US-09-949-016-12505/c
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ORGANISM: Human
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306 ATATTTTGATAATCATTCTAGTGATTTTGAGAAATTCTCTAAAAAGTTCTTGTAAGTTA 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,866
FILING DATE: 30-MAY-1995
                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/08453866
Fatent No. 5756289
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
OORRESPONDENCE 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: LOS Angeles
STREET: CA
                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Wetherell Ph.D., John R.
REGESTRATION NUMBER: 31.678
REFERENCE/DOCKET NUMBER: PD-2458
TELEPHONE: (619) 455-5100
TELEPAX: (619) 455-5100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1689 base pairs
                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/008,001
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1689 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
CLONE: Protein Kinase
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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294..1385
                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY:
; LOCATION:
US-08-447-500-11
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544773 TAATAGACATTTTAAGCACAAGCAAAATTAATATTTGTACCTTTAAATATGATAATGAACT 544714
                                                                                     544713 GAAGCICIATATGCCAATTGTATGATATATCAGCATTCCCATTAAGCACATTCTTCGATA 544654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . LOCATION: (1)..(1141)
. OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters US-09-806-708B-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 TGGCAGTTTACGACAAGGACACCCCGACCGATGGCACAATGTGGCAAAAGCTGTCGGAG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 GGAAAACTGTAGAAGAAGTGAAGCGCCACTATGACATTCTCGTCGAGGATCTCATCAACA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 TCGAGACTGGTCGTGTCCCTTTGCCCAATTACAAGACCTTCGAATCTAACTCAAGAAGCA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 TCAATGACTTTGACACAAGGTATATAACTAAATATCTATATATGATGCTCTCGATATATT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 ITGATAATCATTCTAGTGATTTTGAGAAATTCTCTCAAAAAGTTCTTGTAAGTTATATT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 22. Application US/09806708B
Patent No. 6784342
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REPERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT APPLICATION NUMBER: US/09/806,708B
FILMS APPLICATION NUMBER: US/09/806,708B
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.0
SEQ ID NO 22
LENGTH! 1141
                                              280 AAATATCTATATATGATGCTCTCGATATATTTTGATAATCATTCTAGTGATTTTTGAGAAA
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                                                                                                                                                                              544653 TATTCTGCAAAAGTCTTGGTTCTAAAAGTT 544623
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Patent No. 5627064
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PROTEIN KINASES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
                                                                                                                                    340 ITCICICAAAAGTICITGIAAGTIAITI 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial sequence
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CA
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1554 AAACCCAAATGTCCTTGTTCATATATGTATTGTATTTGTATATACATATATGTGTGT 1613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 AAGCATCAATGACTTTGACACAGGTATATAACTAAATATCTATATATGATGCTCTCGAT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATENT NO. 57,78800.

PAPLICANT: DeMaggio, Anthony J.

APPLICANT: Hoeketra, Merl F.

TITLE OF INVENTION: Materials and Methods Relating to Proteins that
TITLE OF INVENTION: Materials and Methods Relating to Proteins that
TITLE OF INVENTION: Materials and Methods Relating to Proteins that
TITLE OF INVENTION: Materials and Methods Relating to Proteins that
TITLE OF INVENTION: Materials 48

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CONTRY: United States of America
STATE: Illinois
COUNTRY: United States of America
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PRILING DATE: 06-JUN-1995
FILING DATE: 21-JAN-1994
ATPLICATION NUMBER: US 08/184,605
FILING DATE: 21-JAN-1994
ATPLICATION NUMBER: US 08/184,605
FILING DATE: 21-JAN-1994
ATPRIEVARIEV AGENT INFORMATION:
ANAMER NUMBER: METERORAFIED NUMBER: METERORAFIED NUMBER: US 08/184,605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: NO. 5728806and, Greta E.
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 27866/31
TELEPHONE: 312/474-6300
TELEPHONE: 312/474-6300
TELEFAX: 312/474-648
TELER: 25-3856
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 2385 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 41, Application US/08468036 Patent No. 5728806
                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                           TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 2385 base pairs TYPE: nucleic acid STRANNEDNESS: single
   : 312-474-6300
312-474-0448
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297..1388
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US-08-468-036-41
                                                                                                                                                                                                                                                                                                                               ; NAME/KEY:
; LOCATION:
US-08-454-097-9
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US-08-468-036-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 AAGCATCAATGACTTTGACACAAGGTATATAACTAAATATCTATATATGATGCTCTCGAT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 AIAITITGAIAAICAITCIAGIGAITITGAGAAAITCICICAAAAAGITCTIGIAAGITA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
9.7%; Score 36.8; DB 2; Length 1689;
Best Local Similarity 56.7%; Pred. No. 1.1;
Matches 68; Conservative 0; Mismatches 52; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STAKET: 2.33 SOUCH WACKET DIIVE, 530U SEGIES 10WEL
CITY: CLICAGO
STATE: Illinois
COUNTRY: USA
ZUP: 60606-6402
COMPUTER: ELADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TIBM PC COMPACIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,097
FILING DATE: 30-MAY-1995
CLASSIFFCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
APPLICATION NUMBER: US 08/008,001
FILING DATE: 1-JAN-1993
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/008,001
FILING DATE: 31-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5864412and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31853
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08454097
Patent No. 5666412
GENERAL INFORMATION:
APPLICATT: Hoekstra, Merl F.
TITLE OF INVENTION: Protein Kinases
NUMBER OF SEQUENCES: 57
CORRESPONDENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSER: Marchall, O'Toole, Gerstein, Murray & STREET: 233 South Wacker Drive, 6300 Sears Tower
            FILING DATE: 20-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: WECHEFALL Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-2458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5100
SEQUENCE CHARACTERISTICS:
LENGTH: 1689 base pairs
TYPE: nucleic acid
STRANDENES: single
   US 08/008,001
                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
CLONE: Protein Kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: 294..1385
US-08-453-866-11
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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                                                                                                       246 AAGCATCAATGACTTTGACACAAGGTATATAACTAAATATCTATATATGATGCTCTCGAT 305
                                                                                                                                                                                                     306 ATAITITGATAATCATICIAGIGATITITGAGAAATICICICAAAAAGITCTIGIAAGITA 365
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                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Demaggio, Anthony J.
APPLICANT: Hoeketra, Merl F.
TITLE OF INVENTION: Materials and Methods Relating to Proteins
TITLE OF INVENTION: that Interact with Casein Kinase I
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
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O
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0
Query Match
9.7%; Score 36.8; DB 2; Length 2385;
Best Local Similarity 56.7%; Pred. No. 1.3;
Matches 68; Conservative 0; Mismatches 52; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.7%; Score 36.8; DB 2; Length 2385; 56.7%; Pred. No. 1.3; cive 0; Mismatches 52; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 1111nois CUUTRY: United States of America 21P: 60606-6402 COMPUTER READABLE FORM: MEDTUM TYPE: FORD 405 MS COMPUTER: 1BM PC COMPATIBLE OF COMPATIBLE PATENTIN PC-DOS/MS-DOS SOFFWARE: PATENTIN RC-BOS/MS-DOS SOFFWARE: PATENTIN PC-DOS/MS-DOS SOFFWARE: PATENTIN PC-DOS/MS-DOS SOFFWARE: PATENTIN DATA: APPLICATION NUMBER: US/08/376,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/184,605
FILING DATE: 21-JAN-1994
ATTORNEY/AGBNI INFORMATION:
NAME: No. 5846764and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31784
TELECOMMUNICATION INFORMATION:
TELEFAX: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                      US-08-376-843-41
; Sequence 41, Application US/08376843
; Patent No. 5846764
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 2385 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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STRANDEDNESS: single
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Best Local Similarity
Matches 68; Conserv
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1554 AAACCCAAATGTCCTTGTTCATATATATGTATATGTATTTGTATATACATATATGTGTGT 1613
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                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sears Tower CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52; Indels
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,359
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
9.7%; Score 36.8; DE
Best Local Similarity 56.7%; Pred. No. 1.3;
Matches 68; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27866/31853
                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PLICASSIFICATION DATA:
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-7AN-1993
PRIOR APPLICATION NUMBER: US 07/728,783
APPLICATION NUMBER: US 07/728,783
FILING DATE: 03-UUL-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 35,302
TELECHONE: 312-474-6300
TELECHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: March 10, 2006, 18:45:53
Job time : 140 secs
                                                                                                                                                                                               CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATINE
OPERATING SYSTEM: PC-DOS/MS-DOS
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 2385 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297..1388
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; LOCATION:
US-08-185-359-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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model
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using
search,
nucleic
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nucleic
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; Search time 2647 Seconds	(without alignments)	6734.370 Million cell updates/sec
March 10, 2006, 18:32:51		
2006,		
10,		
March		
on:		
Run		

Title: Perfect score: Sequence:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

## Database :

BST:\*
1: 9b\_est1:\*
2: 9b\_est2:\*
3: 9b\_est2:\*
4: 9b\_htc:\*
5: 9b\_est4:\*
6: 9b\_est6:\*
7: 9b\_est6:\*
7: 9b\_est6:\*
7: 9b\_est7:\*
9: 9b\_9ss2:\*
11: 9b\_9ss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		d			Contraction	
Result No.	Score	Ouery Match	o Lery Match Length DB	03	ID	Description
	181	47.5	256	6	CC179487	CC179487 SALK 0699
0	146.8	38.5	793	0	BH947619	BH947619 obu80f11.
m	137.2	36.0	446	80	L38243	L38243 BNAF0581E M
4	128.8	33.8	456	7	C0052301	C0052301 Mdfw2057o
S	124.2	32.6	632	9	CF230621	CF230621 PtaC0010H
9	122.6	32.2	662	7	CV277080	
7	121.8	32.0	728	ß	BU890694	BU890694 P040E03 P
80	121.2	31.8	457	9	CD669972	CD669972 eeplc.pk0
0	121	31.8	516	7	CV278823	CV278823 WS0147.B2
0 10	121	31.8	588	7	CV283381	_
c 11	120.4	31.6	624	7	CV232994	CV232994 WS0199.B2
c 15	120.4	31.6	627		CV230387	CV230387 WS01916.B
13	119.8	31.4	626	ø	CB920052	CB920052 VVD058F11
14	119.8	31.4	662	9	CB919185	CB919185 VVD042D03
12	118.2	31.0	474	Ŋ	BU668323	BU668323 MC01026A1
16	117.8	30.9	349	S	BU822353	BU822353 UB36DPB08
17	117	30.7	513	7	C0997831	CO997831 pam01-16m
18	115.4	30.3	599	æ	CV882244	CV882244 Mdlv3 403
ი 19	115.4	30.3	653	æ	DR997716	DR997716 Mdfb8004M
50	115.4	30.3	629	8	DR990507	DR990507 Mdlr7005H
21	115.4	30.3	099	œ	DR995864	DR995864 Mdas9011J
c 55	115.4	30.3	688	7	CV186968	CV186968 Mdlv2 401
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23 113.6 29.8 629 8 DR994824 24 113.4 29.8 577 1 AJ768009 25 112.4 29.8 577 1 AJ768009 25 112.4 29.5 577 1 AJ768009 26 112.4 29.5 670 2 BG726181 27 111.4 29.2 476 6 CB035850 30 109.8 28.8 492 6 CB002633 31 109.8 28.8 492 6 CB00272 33 109.8 28.8 492 6 CB00272 34 109.8 28.8 513 6 CB34615 35 109.8 28.8 513 6 CB34615 36 109.8 28.8 513 6 CB34516 37 109.8 28.8 513 6 CB34516 38 109.8 28.8 513 6 CB34529 37 109.8 28.8 613 6 CB34529 38 109.8 28.8 613 6 CB345561 38 109.8 28.8 613 6 CB345561 39 109.8 28.8 636 6 CB34383 41 109.8 28.8 636 6 CB34353 42 109.8 28.8 636 6 CB34353 43 109.8 28.8 636 6 CB34353 44 108.8 28.8 655 1 AJ320048 45 108.8 28.6 555 1 AJ320064
24 113.6 29.8 629 25 112.4 29.8 577 26 112.2 29.4 497 27 111.4 29.5 460 28 110.6 29.0 611 29 110.6 29.0 611 30 109.8 28.8 492 31 109.8 28.8 692 34 109.8 28.8 618 35 109.8 28.8 618 36 109.8 28.8 618 37 109.8 28.8 618 36 109.8 28.8 618 37 109.8 28.8 618 38 109.8 28.8 618 39 109.8 28.8 618 40 109.8 28.8 636 41 109.8 28.8 636 41 109.8 28.8 637 42 108.8 28.6 557 44 108.8 28.6 557
23 113 6 29 8 26 112 4 29 5 2 6 112 4 29 5 2 6 112 2 2 2 9 5 2 6 112 2 2 2 9 5 2 6 2 6 2 6 2 6 2 6 2 6 2 6 2 6 2 6 2
23 1113.6 25 1112.4 26 1112.4 27 1111.2 28 110.6 30 100.8 31 100.8 31 100.8 34 100.8 36 100.8 37 100.8 38 100.8 40 100.8 41 100.8 42 100.8 44 100.8
2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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## ALIGNMENTS

CC179487 SALK 069941.39.90.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_069941.39.90.x, genomic CC179487 CC179487.1 GI:30318038 GSS. Arabidopsis thaliana (thale cress)	Atablodysis (maitantes) Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantes, Streptophyta; Emkaryota; Viridiplantes, Spermatophyta; Magnoliophyta; eudicotyledons; cosies; erosids; errosids II; Brassicales; Brassicaceae; Arabidopsis.  1 (bases I to 256) Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Bcker,J.R.	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome (2001) Unpublished (2001) Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGnAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tlel: 858 453 4100 x1752 Fax: 858 558 6379 Email: ecker@salk.edu	This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of AL1975250.  Class TDNA tagged.  Class TDNA tagged.  1256  /organism="Arabidopsis thaliana" /mol type="genomic DNA" /ecctype="genomic DNA" /ecctype="col.o" /db_xref="taxon:3702" /clone="Akabidopsis thaliana TDNA insertion lines" /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can
RESULT 1 CC179487 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE OUTCOM	REFERENCE AUTHORS	TITLE JOURNAL COMMENT	PEATURES SOURCE

US-10-697-787-1 381 1 atggcgtcaaactcaagaag.....gttatattttttggtttaa 381

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

<sup>41078325</sup> segs, 23393541228 residues Searched:

<sup>82156650</sup> Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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CO052301 Mdfw Malus x domestica cDNA clone Mdfw2057018.yl Mdfw Malus x domestica cDNA clone Mdfw2057018 5' similar to TR:Q9SIJ5 Q9SIJ5 ATZG21650 PROTEIN. ;, mRNA sequence. CO052301. GI:48693766
                                                                                                                                                                                                                                                              L38243 446 bp mRNA linear EST 03-JUL-1995
BNAF0581E Mustard flower buds Brassica rapa cDNA, mRNA sequence.
L38243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 GGCAGTTTACGACAAGGACACACCCGACCGATGGCACAATGTGGCAAAAGCTGTCGGAGG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 AGCCGTTTACGACAAAGACACTCCAGACCGTTGGCAAAACGTGGCCCAAAGCCGTCGGGAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 cgagcaagactragitcctritgccraaaracaagaccgrcgargragaaraaarcaag 320
                                          Brassica rapa
Mukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 GAAAACTGTAGAAGAAGTGAAGCGCCACTATGACATTCTCGTCGAGGATCTCATCAACAT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 TAAATCGGCAGAGGAAGTCAAACGTCACTACGATATTCTCGTTGAAGATCTCATGAACAT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGAGACTGGTCGTGTCCCTTTGCCCAATTACAAGACCTTCGA-----ATCTAACTCAAG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 crcaagriciargagciccrcriggacgiciaagcaaaraagararicgaaaggcrir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 446)
Lim,C.O., Kim,H.Y., Kim,M.G., Lee,S.I., Chung,W.S., Park,S.H.,
Hwang,I. and Cho,M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 CTCAAGAAGTTCAATCTCACCATGGACGTTTAGTCAAAACAAGATGTTCGAGAGGGCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                  425 CCTTCGATTCTAACTCAAGAGGCATCAATGACTTCGACACGAGGTATATGCTA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expressed sequence tags of Chinese cabbage flower bud cDNA Plant Physiol. 111 (2), 577-588 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center
                                                                                                           227 CCTTCGAATCTAACTCAAGAAGCATCAATGACTTTGACACAAGGTATATAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 36.0%; Score 137.2; DB 8; Length 446; Best Local Similarity 71.4%; Pred. No. 6.2e-26; Matches 197; Conservative 0; Mismatches 73; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Lim,C.O., Kim,M.G., Hwang,I. and Cho,M.J. Plant Molecular Bloology and Blotechnology Research Email: pmbbrc@nongae.gam.ac.kr. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGCATCAATGACTTTGACACAAGGTATATAACTAA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321 AGGCATCAACGGTTACGGTTTGAGGTTAATGAAAA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol type="manna"
/mol type="manna"
/strain="pekinensis"
/db xref="taxon:311"
/clone lib="Whstard flower buds"
/note="Devel_stage = flower bud"
                                                                                                                                                                                                                                                                                                                                                                              Brassica rapa (Brassica campestris)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Brassica rapa"
                                                                                                                                                                                                                                                                                                                                    L38243.1 GI:887283
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CO052301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BH947619 793 bp DNA linear GSS 01-OCT-2002 obu80f11.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
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                                                                                                                                                                                                                                              61 GAGAGGCCTTGCCAGTTTACGACAAGGACACCCGACGATGCCACAATGTGGCAAAA 120
                                                                                                                                                                                                                                                                                        GCTGTCGGAGGGAAAACTGTAGAAGAAGTGAAGCGCCACTATGACATTCTCGTCGAGGAT 180
                                                                                                                                                                                                                                                                                                                                                                180 GCTGTCGGAGGGAAACTGTATAAGAAGTGAACCGCCTCTATGACATTCTCGTCCAGAA 239
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
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                                                                                                                                                          9
http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                   1 ATGGCGTCAAACTCAAGAAGTTCAATCTCACCATGGACGTTTAGTCAAAACAAGATGTTC
                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 793)
Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shorgun reads from Brassica oleracea
Unpublished (2002)
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                                                               Length 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: obu80 row: f column: 11
Seq primer: -21UPpOT forward
                                                               Score 181; DB 9;
Pred. No. 9.7e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Brassica oleracea"
                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence start: 112
High quality sequence stop: 551.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                             CTCATCAACATCGAGAC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       crcarcaacarccagac 256
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BH947619.1 GI:23427679
                                                            47.5%;
found at
                                                                                      Best Local Similarity 94.9
Matches 187; Conservative
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Matches 157; C
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                                                                 Query Match
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BH947619/c
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were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 4 hours at 30c. Unhybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DHIOB cells to generate the normalized library. The total number of clones with insert was 9x10°6 cfu. Background of empty clones was less than 1%."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                632 bp mRNA linear EST 05-AUG-2003 cDNA library from cambial zone Populus alba 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Populus alba x Populus tremula
Populus alba x Populus tremula
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expressed sequence tags from poplar wood tissues - A comparative analysis from multiple libraries
Plant Biol. 6 (1), 55-64 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 GAGGGCCTTGGCAGTTTACGACAAGGACACCCCGACCGATGGCACAATGTGGCAAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 TGTCGGAGGGAAAACTGTAGAAGAAGTGAAGCGCCACTATGACATTCTCGTCGAGGATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 CGTCGGCGGAAAATCTGCGGAGGAAGTAAAGGGCACTACGAGATTCTGGTGCATGATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GGCGTCAAACTCAAGAAGTTCAATCTCACCATGGACGTTTAGTCAAAACAAGATGTTCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Leple JC
Unit of Forest improvement, Genetics and Physiology
National Institute for Agricultural Research (INRA)
Domaine de Limere, BP20619 ARDON, 45166 OLIVET CEDEX, FRANCE
Tel: 33 02 38 41 78 00
Fax: 33 02 38 41 78 79
Email: Jean-Charles Leple@orleans.inra.fr
                                                                                                                                                                                                                                                                                                                                             Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Populus alba x Populus tremula"
                                                                                                                                                                                                                                                                                                                                                                                                          77; Indels
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BACKWARD: TriplexB 5' ATACGACTCATTATAGGCCGA 3'
Place: PtaCOL10 row: H column: 11
Seq primer: TriplexA 5' CTCGGGAAGCGCCCATTGTG 3'
                                                                                                                                                                                                                                                                                                                                          Query Match
33.8%; Score 128.8; DB 7;
Best Local Similarity 69.4%; Pred. No. 1.1e-23;
Matches 175; Conservative 0; Mismatches 77;
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/strain="clone INRA 717-1-B4"
/db_xref="taxon:80863"
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x Populus tremula cDNA 5'
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CF230621.1 GI:33450050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 CAGCGGCAGCAA 307
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CF230621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Walus x domestica"
/mol type="mRNA"
/cullivar="GoldRush"
/db_rare="acoldRush"
/db_rare="acoldRush"
/db_rare="acoldRush"
/db_rare="acoldRush"
/db_rare="acoldRush"
/db_rare="blower"
/clone_lib="Wdfw%057018"
/tissue type="mRNA was extracted separately from seath acoldrush in the bold of the bold of the balloon, open andafter acoldrush in the Oligotex Direct mRNA was extracted separately from each floral stage (bud, balloon, open andafter acoldrush in the Oligotex Direct mRNA kit (diagen). mRNA was reverse the Oligotex Direct mRNA kit (diagen). mRNA was reverse table below). CONA's from different stages were pooled in equal amounts before adaptor ligation. Tag identification when sequencing from 5' end: Stage 1 (bud) insert 18(A)TGGGA; Stage 2 (balloon) insert 18(A)TGGGA; Stage 2 (balloon) insert 18(A)TGGGA; Stage 1 (bud) insert; Stage 3 (open) ACGCA18(T) insert; Stage 2 (balloon) insert 18(A)TGGGA; Stage 4 (afterpollination) ACGCA18(T) insert; Stage 2 (balloon) TGCGA18(T) insert; Stage 2 (balloon) TGCGA18(T) insert; Stage 3 (open) ACGCA18(T) insert; Stage 4 (afterpollination) ACGCA18(T) insert; Stage 5 (open) ACGCA18(T) insert; Stage 6 (afterpollination) ACGCA18(T) insert; Stage 7 (balloon) TCCGA18(T) insert; Stage 7 (balloon) TCCGA18(T) insert; Stage 7 (balloon) TCCGA18(T) insert; Stage 8 (open) ACGCA18(T) insert; Stage 8 (open) ACGCA18(T) insert; Stage 9 (balloon) TCCGA18(T) insert; Stage 9 (balloon) TCCGA18(T) insert; Stage 9 (balloon) TCCGA18(T) insert; Stage 9 (balloon) ACGCA18(T) AccCA18(T) Acc
                                                                                                                                                                                      E 1 (Dases 1 to 456)

S Korban, S. Vodkin, L. Liu, L. Gasic, K., Gonzales, O., Hernandez, A., Aldwinckle, H., Walnoy, M., Carzoll, N., Goldsbrough, P., Orvis, K., Clifcon, S., Pape, D., Marza, M., Hillier, L., Martin, J., Wylie, T., Dante, M., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Ronko, I. Tsagareishvill, R., Kennedy, S., Waterston, R. and Wilson, R. Apple Functional Genomics grant - NSF 0321702

Longublished (2004)

Longublished (2004)

Apple Functional Genomics grant - NSF 0321702

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800
                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids I, Rosales, Rosaceae, Maloideae, Malus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Library materials provided by: Schuyler S. Korban Library constructed by: A. Hernandez / K. Gasic Library sequenced by: Washington University Genome Sequencing Center Washington University Genome Sequencing Center Seq primer: -40UP from Gibco High quality sequence stop: 456.
      EST.
Malus x domestica
Malus x domestica
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139
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        Populus trichocarpa x Populus deltoides
Populus trichocarpa x Populus deltoides
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
1 (bases 1 to 662)
1 (bases 1 to 662)
1 Kalphy S.; Cooper, D.; Palmquist, D., Stott, J., Barber, S., Yang, G., Rirkpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G., Babakaiff, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A., Mayo, M., Moran, J., Olson, T., Wong, D., Ritland, C.E., Siddiqui, A.,
Bohlmann, J.
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Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                         211 AATTCTCTCACCTCTTGGACACCTAAGCAAAGCAAAGTCTTCGAAAAGGCCCTGGCTTTA 270
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Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 123
'tissue_type="cambial zone harvested on the bark side"
                                                                                                                                                                                                                                                                                                                                                                                          AGTICAATCICACCAIGGACGITIAGICAAAACAAGAIGIICGAGAGGGCCTIGGCAGIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 1-604-822-2114
Email: bohlmann@msl.ubc.ca
Plate: WS0142 row: J column: 13
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Best Local Similarity
Matches 156, Conserva
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CV277080/c
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BU890694 11n-OCT-2002
P040E03 Populus petioles CDNA library Populus tremula CDNA 5 prime,
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Salicaeae; Saliceae; Populus.

1 (bases I to 728)
Unneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
Unneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries
Unpublished (2002)
Contact: BHALERAO RUPALI R.
Unea Plant Science Center
Department of Plant Physiology
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                                                                             organism="Populus trichocarpa x Populus deltoides"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.2%; Score 122.6; DB 7; Length 662; 74.2%; Pred. No. 5.5e-22; ive 0; Mismatches 54; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 GGTCGTGTCCCTTTGCCCAATTACAAGAC 227
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High quality sequence stop: 662
POLYA=Yes.
                                                                                                                                     /db_xref="taxon:3695"
/clone="WS0142_J13"
                                      location/Qualifiers
                                                                                                /mol_type="mRNA"
/cultivar="H11-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
BU890694
BU890694.1 GI:24101759
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                                                                                                                                                                              /sex="Male"
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Populus trichocarpa x Populus deltoides
Populus trichocarpa x Populus deltoides
Bugaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bugaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Tosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
I (bases I to 516)
Kirkpatrick, Rooper, D., Kolosova, N., Oddy, C., Butterfield, Y.,
Kirkpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G.,
Babakaiff, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A.,
Mayo, M., Moran, J., Olson, T., Wong, D., Ritland, C.E., Siddigui, A.,
Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritland, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               516 bp mRNA linear EST 22-SEP-2004 WS0147.B21_III PTXD-IL-A-5 Populus trichocarpa x Populus deltoides CV278823
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Unpublished (2004)
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      /note="Vector: pBluescript SK+; Site 1: EcoRI; Site_2:
XhoI; Eucalyptus grandis leaves/petioles/stems"
                                                                                                                                                                           28 TCACCATGGACGTTTAGTCAAAACAAGATGTTCGAGAGGGCCTTGGCAGTTTACGACAAG
                                                                                                                                                                                                                                                           88 GACACACCCGACCGATGGCACAATGTGGCAAAAGCTGTCGGAGGGAAAAACTGTAGAAGAA
                                                                                                                                                                                                                                                                                          Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 123
Tel: 1-604-822-0282
                                                                                                                                     Gaps
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/organism="Populus trichocarpa x Populus deltoides"
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                                                                                           457;
                                                                                           Length
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                                                                                      Score 121.2; DB 6;
Pred. No. 1.2e-21;
0; Mismatches 68;
                                                                                                                                 0; Mismatches
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/cultivar="H11-11"
/db_xref="taxon:3695"
/clone="WS0147_111"
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Plate: WS0147 row: I column: 1
High quality sequence stop: 516
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                                                                                      Query Match
Best Local Similarity 70.4%;
Matches 162; Conservative
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CV278823/c
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                                                                                                                                                                                                                                                                                                                                                                                                     257 TCAAATGGCTCCGGCTCCTCGACAGCAACAAAAAAAAGAAGCTATTCGAGAAGGCCCTG 316
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons; core eudicotyledons; rosids, Myrtales, Myrtaceae, Eucalyptus.

1 (bases 1 to 457)
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                                                                                                                                                                                                                                                                                                                            Gaps
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Bucalyptus EST Project
Unpublished (2001)
Contact: Scott V. Tingey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
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                                                                                                                                                                                                                                                                                  Length 728
                                                                                                    1...728
/organism="Populus tremula"
/mol_type="mxnn."
/db_xref="taxnn."
/tissue_type="petioles"
/clone_lib="Populus petioles cDNA library"
                                                                                                                                                                                                                                                                           Query Match
32.0%; Score 121.8; DB 5; Length
Best Local Similarity 68.6%; Pred. No. 9.2e-22;
Matches 168; Conservative 0; Mismatches 77; Indels
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/mol_type="mRNA"
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/clone="eeplc.pk005.g21"
/tissue_type="leaf"
/lab host="PH108"
/clone_lib="eeplc"
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupail.bhalcrao@plantphys.umu.se.
Location/Qualifiers
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Email: Scoct.V.Tingey@USA.dupont.com
Seq primer: M13.
Location/Qualifiers
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CD669972
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Hubner (forest tent caterpillar) mid-instar larvae caged on the sapling using mesh bags. Mature leaves from within the caged regalon were collected 2 hours, 12 hours, 24 hours, 24 hours and 48 hours after the onset of treatment. mRNA was isolated from each tissue source independently and equal quantities of mRNA from each tissue were then pooled. CDNA was prepared from 5 micrograms of mRNA and directionally ligated into the pBluescript II SK (+) XR vector using the pBluescript II XR cDNA library Construction Kit according to manufacturer's instructions with modifications (Stratagene). Plasmid DNA was then transformed by electroporation into DH108 cells (Invitrogen) for
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Populus trichocarpa x Populus deltoides
Populus trichocarpa x Populus deltoides
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
1 (Bases I to 58D)
Kalph,S., Cooper,D., Kolosova,N., Oddy,C., Butterfield,Y.,
Kirkpatrick,R., Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G.,
Babaakaiff,R., Brown-John,M., Chand,S., Featherstone,R., Masson,A.,
Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddiqui,A.,
Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., Ritland,K. and
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The poplar transcriptome: Analysis of expressed sequence tags from multiple CDNA libraries
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481 AATTCTCTCACCTCTTGGACACCTAAGCAAACAACTATTCGAAAAGGCCCTGGCTTTA 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTAGAAGAAGTGAAGCGCCACTATGACATTCTCGTCGAGGATCTCATCAACATCGAGACT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 GCAGAGGAAGTGAAGAGGCACTATGAGATTCTCATCAAGGATGTCAGGGAAATTGAGTCT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78
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University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, Eritish Columbia, Canada, V6T 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 TACGACAAGGACACCCCGACCGATGGCACAATGTGGCAAAAGCTGTCGGAGGGAAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 AGTICAATCICACCAIGGACGITTAGICAAAACAAGAIGITCGAGAGGGCCTIGGCAGIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.8%; Score 121; DB 7; Length 516; 73.7%; Pred. No. 1.4e-21; ive 0; Mismatches 55; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAGAGTTCCATTCCCTAATTACAGGTC 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 588 POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               row: C column:
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Email: bohlmann@msl.ubc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CV283381.1 GI:52536356
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                                                                                                                                                                                                                                                                                                                                                                                            propagation."
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Best Local Similarity
Matches 154; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139
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KEYWORDS
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ò 셤 ઠે /organism="Populus trichocarpa x Populus deltoides"

Location/Qualifiers

FEATURES

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/lab host="E. coli DH10B T1 phage resistant cells"
/clone lib="PTxD-IL-N-A-9"
/note="Weator: pBluescript II SK (+) XR; Site 1: EcoRI (5'
end of cDNA); Site 2: Xhoi (3' end of cDNA); Sapling trees
two metres in height and grown under greenhouse conditions
were exposed to continuous feeding by Malacosoma disstria
Hubner (forest tent caterpillar) mid-instar larvae caged
on the sapling using mesh bags. Mature leaves from within
the caged region were collected 2 hours, 12 hours, 24
hours and 48 hours after the onset of treatment. mRNA was
isolated from each tissue source independently and equal
quantities of mRNA from each tissue were then pooled. cDNA
was prepared from S micrograms of mRNA and directionally
ligated into the pBluescript II SK (+) XR vector using the
pBluescript II XR ONNA tibrary Construction Kit according
to manufacturer's instructions with modificants.
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WS0199_E24 3', mRNA sequence.
CV232994
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Ralph, S., Cooper, D., Kolosova, N., Oddy, C., Butterfield, Y.,
Kirkpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G.,
Babakaiff, R., Brinn, John, M., Chand, S., Featherstone, R., Masson, A.,
Mayo, M., Moran, J., Olson, T., Wong, D., Ritland, C.E., Siddiqui, A.,
Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritland, K. and
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Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 TACGACAAGGACACCCCGACCGATGGCACAATGTGGCAAAAGCTGTCGGAGGGAAAACT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 GTAGAAGAAGTGAAGCGCCACTATGACATTCTCGTCGAGGATCTCATCAACATCGAGACT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Populus trichocarpa
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312 GCAGAGGAAGTIGAAGAGGGCACTATCAGATTCTCATCAAGGATGTCAGGGAAATTGAGTCT 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGTICAATCICACCATGGACGITIAGICAAAACAAGAIGTICGAGAGGGCCTIGGCAGTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Stratagene). Plasmid DNA was then transformed by electroporation into DH10B cells (Invircogen) for propagation. Normalization was applied according to published methods [Bonaldo M.F. et al. (1996) Genome Research 6(9):791] in order to reduce the abundance
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31.8%; Score 121; DB 7; Length 588;
Best Local Similarity 73.7%; Pred. No. 1.5e-21;
Matches 154; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      highly expressed transcripts.
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/db_xref="taxon:3695"
/clone="WS0187_C24"
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                                                                        /sex="Male"
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CV232994/c
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    SOURCE
ORGANISM
                                                                                                                       REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                            TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /Jab host-"E. coli DH10B T1 phage resistant cells"
/Jab host-"E. coli DH10B T1 phage resistant cells"
/Jobe = 11b="PT-DX-N-A-10"
/Jobe = 12b="Vector: pBluescript I1 SK (+) XR; Site 1: EcoRI (5')
end of cDNA); Site = 2: XhoI (3' end of cDNA); Outer xylem
from 5 year old trees harvested every two weeks between
April and October of 2002 at the University of British
Columbia south campus farm in Vancouver. British Columbia
and equal quantities of mRNA from each tissue were then
pooled. cDNA was prepared from 5 micrograms of mRNA and
directionally ligated into the pBluescript I1 SK (+) XR
vector using the pBluescript II XR cDNA Library
Construction Kit according to manufacturer's instructions
with modifications (Stratagene). Plasmid DNA was then
transformed by electroporation into DH10B cells.
// Town town of the correspondence of the columbiant transformed by electroporation into DH10B cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Invitrogen) for propagation. Normalization was applied according to published methods (Bonaldo M.F. et al. (1996) Genome Research 6(9):791] in order to reduce the abundance of highly expressed transcripts."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 ACATCGAGACTGGTCGTGTCCCTTTGCCCAATTACAAGACCTTCGAATCTAACTCAAAAA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    385 ACATAGAATCCGGCCAAGCCCCTCTGCCGAATTACAAGCCCTTGGCAGCAATGGTAGA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            445 GTGGCAAGTCTCCTGAAGAAGTTAAGAGGCACTATGATCGTCTCGTGGAGGATCTCGTGT 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAACTCAAGAAGTTCAATCTCACCATGGACGTTTAGTCAAAACAAGATGTTCGAGAGGG 67
                                                                          Boulevard, Rm. 237,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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CV230387
CV230387.1 GI:52383831
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                   Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Bou
Vancouver, British Columbia, Canada, V6T 123
Tel: 1-664-822-2082
Fax: 1-664-822-214
Email: bohlmann@m81.ubc.ca
Place: W80199 row: E column: 24
High quality sequence stop: 624
POLYA=Yes.
                                                                                                                                                                                                                                                                                                             /organism="Populus trichocarpa"
                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:3694"
/clone="WS0199_E24"
/sex="Not_determined"
                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/cultivar="VT-125"
  Contact: Joerg Bohlmann
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flone="Vector: pBluescript I3 SK (+) XR; Site 1: EcoRI (5'
end of cDNA); Site 2: Xhol (3' end of CDNA); Outer xylem
from 5 year old trees harvested every two weeks between
April and October of 2002 at the University of British
Columbia south campus farm in vancouver. British Columbia.
mRNA was isolated from each tissue source independently
and equal quantities of mRNA from each tissue were then
pooled. cDNA was prepared from 5 micrograms of mRNA and
directionally ligated into the pBluescript I1 SK CDNA Library
Construction Kit according to manufacturer's instructions
with modifications (Stratagane). Plasmid DNA was then
transformed by electropostation into DH10B cells
Populus trichocarpa (Populus balsamifera subsp. trichocarpa)
Populus trichocarpa
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Trachoophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Trachoophyta;
Tosida; eurosida I; Malpighiales; Salicaceae; Saliceae; Populus.
I (bases 1 to 627)
Ralph,S., Cooper,D., Kolosova,N., Oddy,C., Butterfield,Y.,
Kirkpatrick,R., Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G.,
Babadxiff,R., Brown-John,M., Chand,S., Featherstone,R., Masson,A.,
Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddigui,A.,
Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddigui,A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 123
Tel: 1-604-822-0282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 CAAACTCAAGAAGTTCAATCTCACCATGGACGTTTAGTCAAAACAAGATGTTCGAGAGGG
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Plate: WS01916 row: F column:
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Unpublished (2004)
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                                                     EST 25-APR-2003
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An expressed sequence tag database for abiotic stressed berries of Vitis vinifera var. Chardonnay
Unpublished (2002)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
Was200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
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                                                                                                                                                                                      Vitis vinifera
Vitis vinifera
Vitis vinifera
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
rosids; Vitaceae; Vitis.
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                                                                   VVD042D03_349003 An expressed sequence tag database for abiotic stressed berries of Vitis vinifera var. Chardonnay Vitis Vinifera cDNA clone VVD042D03 5, mRNA sequence.
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Pred. No. 3.1
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High quality sequence stop: 662.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORWARD: T3 20mer
BACKWARD: T7 21mer (backward)
Plate: 042 row: D column: 03
Seq primer: T3 20mer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRimers
                                                                                                                                                   CB919185.1 GI:30133846
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ilarity 70.5%;
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BU668323
                RESULT 14
CB919185
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ECORI; Site_2: Xho!"
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Vitis vinifera
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (basea I to 626)
Cushman,J.C.
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389 ACATAGAATCCGGCCAAGCCCCTCTGCCGAATTACAAGCCCTCTGGCAGCAATGGTAGAG 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    An expressed sequence tag database for abiotic stressed berries (Vitis vinifera var. Chardonnay Unpublished (2002)
Contact: Cushman JC
Department of Biochemistry
University of Nevada MS200, Reno, WN 89557-0014, USA
Tel: 775-784-1918
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Pred. No. 3.1e-21;
0; Mismatches 67; Indels 0
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BACKWARD: T7 21mer (backward)
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Seg primer: T3 20mer
High quality sequence stop: 626.
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PRimers
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
afterids; lamiids; Lamiales; Pedaliaceae; Sesamum.
1 (Dases 1 to 474)
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                                                                                                                                                                         Comparative analysis of Expressed Sequence Tags between Sesamum indicum and Arabidopsis thaliana developing seeds Unpublished (2003)
Unpublished (2003)
Contact: Suh, Mi Chung
Graduate School of Biotechnology, Korea University
1, 5-Ka, Anam-dong, Sungbuk-ku, Seoul 136-701, Rep. of Korea Tel: 82 2 3290 3169
Tex: 82 2 927 9028
Email: michung@korea.ac.kr
Plate: 026 row: A column: 10.
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| forgatism="seamum indicum"
| forgatism="seamum indicum"
| mol_type="mRNA"
| mol_type="mRNA"
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| forl_line="Yangbaeck"
| dev_teqge="5 to 25 days after flowering"
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transgenic plant; peronospora parasitica resistant; PPR2;
pathogen resistant phenotype; modified pathogen resistance; thale cress;
gene; ds.
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                                                                                                                                                                                                                                                                                                                                Thale cress peronospora parasitica resistant protein coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New transgenic plants with increased resistance to pathogens due to altered expression of Peronospora Parasitica Resistant gene (PPR2), useful for generating plants with a pathogen resistance phenotype.
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       ADD30327
ADA256
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P-PSDB; ADF43566.
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                                                                                                                                                                                                                                                                                 This invention relates to a novel plant transcription factor polypeptides, the DNA sequences which encode them and their use in creating transgenic plants. The transgenic plant and methods are useful for producing commercially or agriculturally useful plants having improved tolerance to drought, shade and low nitrogen conditions when compared to wild-type reference plants. The present sequence is that of plant transcription factor gene which was used during the development of
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Creelman RA, Ratcliffe OJ, Canales
Gutterson NI, Reuber TL, Pineda O;
Keddie JS, Jiang C, Century KS, <sup>2</sup>
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Pred. No. 6.2e-68;
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Matches 277; Conservative 0
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      Heard JE, Riechmann JL, Repetti P, Kumimoto RW, Sherman BK, Morrison TA, Zhang JZ, Hempel FD, Li
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                                         The invention relates to a transgenic plant that possesses a plant transformation vector comprising a nucleotide sequence that encodes a peronospora parasitica resistant (FPR2) protein, or a PPR2 orthologue. The transgenic plant is useful in generating plants with a pathogen resistance phenotype. The PPR2 nucleic acids and proteins of the invention are useful in the generation of genetically modified plants having a modified pathogen resistance phenotype. The present DNA sequence encodes an Arabidopsis thaliana PPR2 protein of the invention.
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                                                                                                                                                                                                                                                                   Length 381;
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                             Sequence 381 BP; 122 A; 76 C; 76 G; 107 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                100.0%; Score 381; DB 10;
100.0%; Pred. No. 1.2e-98;
ative 0; Mismatches 0;
        SEQ ID NO 1; 36pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTIATATITCTITGGITIAA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MEND-) MENDEL BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-NOV-2003; 2003US-00714887.
05-DEC-2003; 2003US-0527658P.
05-FEB-2004; 2004US-0542928P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-NOV-2004; 2004WO-US037584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEA27134 standard; DNA; 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stress tolerance; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                       Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transcription factor;
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                                                                                                                                                                                                                                                                                       Local
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18-SEP-2002; 2002US-0411837P.

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CTCATCAACATCGAGACTGGTCGTGTCCCTTTGCCCAATTACAAGACCTTCGA-----A 234
                                                                                                                                                                                                                                                                                                                                                                                                   Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                       271
                                                                                                             241 AGTAAATCTAGAGGCATCGATGATTTTGATTTTGAGGT 277
                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana DNA fragment SEQ ID NO: 5783.
                                                                                     235 TCTAACTCAAGAAGCATCAATGACTTTGACACAAGGT
                                                                                                                                                                                                                                   AAC34192 standard; DNA; 478 BP
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99US-0123180P.
99US-0123548P.
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99US-0132487P.
99US-0132863P.
99US-0134256P.
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99US-0134219P.
99US-0134221P.
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990S-0135124P.
990S-0135353P.
990S-0135629P.
990S-0136021P.
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99US-0134768P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-FEB-2000; 2000EP-00301439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0138540P
                                                                                                                                                                                                                                                                                                                     17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-013
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    181
                                                                                                                                                                                                                                                                             AAC34192;
                                                                                                                                                                                          RESULT 4
AAC34192
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                                                                                                                          유
                                                                                                                                                                                                                                                                                                                                             The present invention relates to novel plant transcription factor proteins (1) and mucleotide sequences (II) (AD06154-AD06774). The sequences can be used to produce transgenic plants which overexpress (II), where the transgenic plant has an altered trait as compared to a nattered trait selected from increased tolerance to abiotic stress, on altered trait selected from increased tolerance to abiotic stress, increased tolerance to cold, increased tolerance to cold, increased tolerance to cold, increased tolerance to cold, increased tolerance to compared tolerance to low increased tolerance to will toler tolerance to will tolerance to will toler tolerance to will tolerance to will toler tolerance to will toler tolerance to will tolerance to will toler tolerance tolerance and particularly to ABA, reduced sensitivity to ACC, altered sense desirity, altered tolerance aboon/nitzgen sensing, early flowering, altered factor morphology, altered vascular tissue structure, altered tolerance altered tolerance, altered trachome structure, altered trachome structure, altered tolerance, altered trachome structure, altered tolerance, altered trachome structure, altered seed factorance, altered trachome structure, altered seed development, altered benefit tolerance, altered trachome structure, altered trachome structure, altered tolerance toleran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGAGGGCCTTGGCAGTTTACGACAGGACACCCGGACCGATGGCACAATGTGGCAAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GAGAGGCTTTAGCCGTTTACGATAAAGACACTCCCGACCGTTGGCAAAACGTGGCTAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGTCGCAGGAAAACTGTAGAAGAAGTCAAGAGCCCACTATGACATTCTCGTCGAGGAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GCAGTTGGAAGTAAATCTGCAGAGGAAGTTAAACGTCACTACGACATCCTCGTTGAAGAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Arcsccrcragricrarcascrccascrcrrcrrcsaccrcraascaaacaacarcrrc 60
                                                                                                                                                                                                                           New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGGCGTCAAACTCAAGAAGTTCAATCTCACCATGGACGTTTAGTCAAAAAAAGATGTTC
                                                                                                         Reuber TL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tch 39.2%; Score 149.4; DB 12; Length 279; al Similarity 74.0%; Pred. No. 1.7e-32; 205; Conservative 0; Mismatches 66; Indels 6;
                                                                                                       Adam LJ, R
Sherman BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,7e-32;
es 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 279 BP; 86 A; 56 C; 65 G; 72 T; 0 U; 0 Other;
                                                                                                    Jiang C, Heard JE, Ratcliffe O, Creelman RA, Riechmann JL, Haake V, Dubell AN, Keddie JS,
                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 509; 510pp; English.
                                                        (MEND-) MENDEL BIOTECHNOLOGY INC.
17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
                                                                                                                                                             WPI; 2004-330163/30.
P-PSDB; ADO62043.
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Matches 205; Conserv
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0.AUG-199 1.AUG-199 2.AUG-199 3.AUG-199 6.AUG-199 6.AUG-199 0.AUG-199 0.AUG-199 3.AUG-199	6 - AUG - 19 7 - AUG - 19 7 - AUG - 19 7 - AUG - 19 8 - A	0007-199 0007-199 0007-199 0007-199 0007-199 0007-199 0007-199 0007-199 0007-199 0007-199
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6; Gaps

25 ATCTCACCATGGACGTTTAGTCAAACAAGATGTTCGAGAGGGCCTTGGCAGTTTACGAC 84

Query Match 36.4%; Score 138.6; DB 3; Length 478; Best Local Similarity 73.4%; Pred. No. 2.6e-29; Matches 193; Conservative 0; Mismatches 64; Indels 6;

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                                                                                                                                                                                         GTACCTTTGCCTAAATACAAAACCGTCGATGTTGGAAGTAAATCTAGAGGAATCAATGAT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene; ss; plant; transcription; gene regulation; gene expression;
transgenic plant; drought resistance; disease resistance; salt tolerance;
cold tolerance; freezing tolerance; flowering; flavor enhancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to novel isolated plant nucleic acid molecules, or variants thereof, that encode transcription factors. Specifically, it refers to transcription factor proteins that are capable of binding to DNA in order to regulate gene transcription and gene expression in a plants, in particular Eucalyptus grandis and pinus radiata. The present invention describes DNA constructs containing DNA encoding a transcription factor that regulates the promoter, which is operably linked to the desired nucleic acid to be expressed. It further provides transgenic plants expressing a transcription factor that confers a trait to the plant such as increased drought, salt or disease tolerance, height nutritional characteristics, as well as improved taste, starch composition, flower longevity and germination, amongst others.

Accordingly, such plants that are successfully transfected with a DNA
                                AAGGACACACCCGACCGATGGCCACAATGTGGCCAAAAGCTGTCGGAGGGAAAACTGTAGAA 144
                                                                                            GAAGTGAAGCGCCACTATGACATTCTCGAGGATCTCATCAACATCGAGACTGGTCGT 204
                                                                                                               62 AAAGACACTCCCGACCGTTGGCAAAACGTCGCTAAAGCAGTTGGAAGTAAATCTGCAGAG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides isolated from plants encoding transcription factors, and polypeptides encoded by such polynucleotides, useful for regulating gene transcription and gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Σ
2 AGCTCTTCTTGGACGTCTAAGCAAAACAAGATGTTCGAGAGGGCTTTAGCCGTTTACGAT
                                                                                                                                                         GTCCCTTTGCCCAATTACAAGACCTTCGA-----ATCTAACTCAAGAAGCATCAATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       iJ, Frost MJ;
Lund ST, Magusin A;
| C, Gause K, Wood |
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eucalyptus grandis transcription factor cDNA MYB family Seq 306.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Emerson SJ,
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Higgins C, Las
Veerakone S,
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                                                                                                                                                                                                                           TTTGACACAGGTATATAACTAA 281
                                                                                                                                                                                                                                                         rtrgartrgaggtrartgaagaa 264
                                                                                                                                                                                                                                                                                                                                            BP
                                                                                                                                                                                                                                                                                                                                         ADW16587 standard; cDNA; 482
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Forster RLS, Grigor M,
Phillips J, Puthigae S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ARBO-) ARBORGEN LLC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eucalyptus grandis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          flower color.
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                                                                                                                                                                                   87
construct can be characterized by a difference in flower color, petal or leaf shape and size, aroma or plant height. This polynucleotide is a plant transcription factor cDNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a recombinant polynucleotide comprising any of the 58798 Cotton plant cDNA sequences mentioned in the specification. Also a recombinant polypeptide comprising any of the 58798 amino acid sequences mentioned in the specification and producing a plant having an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cotton, 88; plant, cold tolerance; growth rate; cell cycle pathway; drought tolerance; plant disease resistance; galactomannan; lignin; plant growth regulator; heat tolerance; herbicide tolerance; homologous recombination; extreme osmotic condition tolerance; pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant nucleic acid molecules and polypeptides from Gossypium hirsutum, useful for producing plants with improved biological characteristics (e.g. improved plant cold or drought tolerance).
                                                                                                                                                                                                                                                                                                                           TCACCATGGACGTTTAGTCAAACAAGATGTTCGAGAGGGCCTTGGCAGTTTACGACAAG
                                                                                                                                                                                                                   64 rcarccriscacicceaascascaacaacaacarcriscaaaaccarrisccrcaarararaacaas
                                                                                                                                                                                                                                                       88 GACACACCCGACCGATGGCACAATGTGGCAAAAGCTGTCGGAGGGAAAACTGTAGAAGAA
                                                                                                                                                                                                                                                                                         184 GTGAAAAGACACTATGAAATTTTAATCGAGGACGTCAAGCACATCGAGTCTGGCAGAGTT
                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                       244 CCTTTTCCTAATTACAGGTCGAGCAACAATAGCGGCTGAAGGTTCGGTGA 293
                                                                                                                                                                                                                                                                                                                                                                                                     208 CCTTTGCCCAATTACAAGACCTTCGAATCTAACTCAAGAAGCATCAATGA
                                                                                                           DB 14; Length
                                                                       Sequence 482 BP; 137 A; 89 C; 121 G; 135 T; 0 U; 0 Other;
                                                                                                                                               Indels
                                                                                                       Query Match 32.2%; Score 122.8; DB 14; Best Local Similarity 70.9%; Pred. No. 8.5e-25; Matches 163; Conservative 0; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 270; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cotton cDNA sequence, SEQ ID 270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADR59489 standard; cDNA; 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAY-2001; 2001US-00849529.
12-DEC-2001; 2001US-00021323.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KOVA/) KOVALIC D K. (ZHOU/) ZHOU Y. (CAOY/) CAO Y.
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                                                                                                                                                                                 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADR59489;
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comprises transforming a plant having an improved property
comprises transforming a plant with a recombinant construct comprising a
promoter region functional in a plant cell operably joined to a
promoter region functional in a plant cell operably joined to a
polynucleotide comprising a coding sequence for a polypeptide associated
with the property, and growing the transformed plant. The polypeptide is
compared to a plant cold tolerance, manipulating growth rate in
plant cells by modification of the cell cycle pathway, improving plant
corpushing galactomannan for lighin or plant growth regulators, improving
plant theat tolerance, improving plant tolerance to plant disease,
corpushing plant conditions or lighin or plants, improving plant tolerance
the rate of homologous recombination in plants, improving plant tolerance
corpustions are and/or uptable with a plants, improving plant tolerance
corpusphorus use and/or uptable, or improving yield by modification of photosynthesis, or improving yield by providing improved
corpusphorus use and/or uptable, or improving yield by providing improved
corpusphorus use and/or uptable, or improving yield by providing improved
corpusphorus use and/or uptable, or improving yield by providing improved
corpusphorus use and/or uptable at least one stress condition. The
polynucleotide and polypeptide may also be used in recombinant DNA
content plant connet form plant connection. NOTE: The sequence data for this
corpusphorus tolerance the printed specification, but was obtained
in all polynomic formar directly from IRDPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 CATGGACAGCCAAGCAAACAAAGATTTCGAAAGGGCTTTAGCTGTTTACGACAAGGACA 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 AGCGCCACTATGACATTCTCGTCGAGGATCTCATCAACATCGAGACTGGTCGTGTCCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATGGACGTTTAGTCAAAACAAGATGTTCGAGAGGGCCTTGGCAGTTTACGACAAGGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in electronic format directly from USPTO at segdata.uspto.gov/sequence.html?Doc1D>20040181830. However only 6585 polynuclectide sequences were available, the remaining 55213 polynuclectides and all 58798 protein sequences were not present.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.7%; Score 120.6; DB 1.75.4%; Pred. No. 4.3e-24; tive 0; Mismatches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 TGCCCAATTACAAGACCTT 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACN61386 standard; cDNA; 543 BP.
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Cotton; plant; EST; expressed sequence tag; transgenic plant; gynoecium; variety Nucotton318; library LIB329; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.
                                                                                           Cotton gynoecium tissue EST Clone ID: LIB3829-015-Q1-N6-E2, SEQ:16167.
                                                                   02-DEC-2004 (first entry)
                                                                                                                                                                                           Gossypium hirsutum
                                                                                                                                                                                                                       US2004123340-A1.
                                                                                                                                                                                                                                               24-JUN-2004
                                         ACN61386;
ACN61386/c
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RESULT 8 ADRS9490

12-DEC-2001; 2001US-00021323. 14-DEC-2000; 2000US-0255619P.

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The invention relates to 17880 cotton expressed sequence tags (ESTS;

ACN45220-ACN63099). The ESTS were isolated from CDNA libraries generated

Erom primed or non-primed seeds from variety DBFS0B, mature seeds from

variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium

tissue, developing fibree, carpel walls and septa from variety

C tissue, developing fibree, carpel walls and septa from variety

Nucotton33B. The invention also relates to substantially purified

proteins or their fragments encoded by nucleic acid molecules of the

invention, and to transformed plants having a nucleic acid construct

comprising a nucleic acid of the invention. The cotton ESTs are useful

comprising a nucleic acid of the invention. The cotton ESTs are useful

comprising a nucleic acid of the invention. The cotton ESTs are useful

comprising a nucleic acid of the invention. The cotton ESTs are useful as

consistent gene function and to determining whether genes

consistent genes function and to determining whether genes

associated with plant growth, quality, yield, and could also serve as

links in metabolic and catabolic pathways. The nucleic acid molecules are

also useful for identifying genes important in initiating and maintaining

ceed germination or the may be used to mitigate stresses encountered

during seed germination. The ESTs additionally enable the acquisition of

promoters and cis-regulatory elements which will be useful to express

cand also permits the acquisition of molecular markers useful in breeding

cand also permits the acquisition of molecular markers useful in breeding

significant genes. The nucleic acid molecules are further useful for

and also permits the acquisition of molecules markers useful in breeding

cathemes, genetic and molecular mapping, and in cloning of agronomically

cathemes and cather or and molecules and molecules are further useful to express
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cotton variety Nucotton33B gynoecium tissue cDNA library (LIB3829). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at seqdata.uspto.gov/sequence.html?DocID=US20040123340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               505 CATGGACAGCCAAGCAAACAAAGATTTCGAAAGGGCTTTAGCTGTTTACGACAAGGACA 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caccadarcerrideracaarerrecraaderreregeadadaaacrerreadaderea 386
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                                                                                                                                                                                                                                       New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 CATGGACGTTTAGTCAAAACAAGATGTTCGAGAGGCCCTTGGCAGTTTACGACAAGGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.2%; Score 119; DB 13; 74.9%; Pred. No. 1.1e-23; ive 0; Mismatches 50;
                                                                                                                                               Ziegler
                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 16167; 34pp; English.
                                                                                                                                               Fincher KL,
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                                                                                                                                               Feng PCC,
                  DEIKMAN J.
FENG P C C.
FINCHER K L.
ZIEGLER T E.
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                                                                                                                                                                                                  WPI; 2004-479808/45.
                                                                                                                                                                                                                                                                                                                               tags to map genes.
                                                                                                                                               Deikman J,
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                     (DEIK/)
(FENG/)
                                                                     (FINC/)
(ZIEG/)
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ADR59490 standard; cDNA; 779
  02-DEC-2004
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The invention relates to a recombinant polynucleotide comprising any of the 58798 Cotton plant cDNA sequences mentioned in the specification.

Also a recombinant polypeptide comprising any of the 58798 amino acid sequences mentioned in the specification and producing a plant having an improved property.

Comprises transforming a plant with a recombinant construct comprising a promoter region functional in a plant call operably joined to a promoter region functional in a plant call operably joined to a promoterry, and growing the transformed plant. The polypeptide is could be improving plant cold tolerance for a polypeptide associated useful for improving plant cold tolerance, manipulating growth rate in plant tolerance, providing increased resistance to plant disease, producing galactomannan (or lignin or plant growth regulators), improving plant tolerance to improving plant tolerance to producing galactomannan (or lignin or plant growth regulators), improving plant tolerance to methodicides, increasing conducing galactomannan (or lignin or plants; improving plant tolerance to extreme commologue recombination in plants; improving plant folerance to extreme commologue recombination in plants; improving plant colerance to extreme commologue, improving yield by modification of such pathogens or pests, improving yield content, improving yield by modification of extrance improving yield by modification of extrance improving yield or improved to extrance for content, improving yield by modification of extrancy improved imp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or phosphorus use and/or uptake, or improving yield by providing improved plant growth and development under at least one stress condition. The polymucleotide and polypeptide may also be used in recombinant DNA constructs, in physical arrays of molecules, as plant breeding markers, or in computer based storage and analysis systems. The present sequence is a Cotton plant cDNA of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant nucleic acid molecules and polypeptides from Gossypium hirsutum, useful for producing plants with improved biological characteristics (e.g. improved plant cold or drought tolerance).
                                                                                                                                                                                                                                 Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway; drought tolerance; plant disease resistance; galactomannan; lignin; plant growth regulator; heat tolerance; herbicide tolerance; homologous recombination; extreme osmotic condition tolerance; pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 segdata.uspto.gov/sequence.html?DocID=20040181810. However only 6585 polynucleotide sequences were available, the remaining 52213 polynucleotides and all 58798 protein sequences were not present.
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                                                                                                                Cotton cDNA sequence, SEQ ID 271.
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12-DEC-2001; 2001US-00021323
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(first entry)
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(ZHOU/) ZHOU Y.
(CAOY/) CAO Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stress resistance,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2004181830-A1.
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31.2%; Score 119; DB 13; Length 779;

Query Match

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                                                                                                                                                                              211
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                                                                               172 CATGGACAGCCAAGCAAAACAAAGATTTCGAAAGGGCTTTTAGCTGTTTACGACAAGGACA 231
                                                                                                               151
                                                                                                                                              291
                                                                                                                                                                                                             292 AGAAGCACTATGAGCTTCTTCAAGATGTTAGACGCATCGAGTCGGGTCGGGTTCCTT 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office a polymucleotide ftp. sequence.html?DocID:3004034888. The polymucleotide of the invention are also useful in physical arrays of molecules and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotific condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                 CATGGACGTTTAGTCAAAACAAGATGTTCGAGAGGCCCTTGGCAGTTTACGACAAGGACA
                                                                                                               92 CACCCGACCGATGGCACAATGTGGCAAAAGCTGTCGGAGGGAAAACTGTAGAAGAAGTGA
                                                                                                                                            232 CACCAGATCGTTGGTACAATGTTGCTAAAGCTGTGGGAGAGAAACTGTTGAGGAAGTGA
                                                                                                                                                                              152 AGCGCCACTATGACATTCTCGTCGAGGATCTCATCAACATCGAGACTGGTCGTGTCCCTT
                  Gaps
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                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tabaska JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant full length insert polynucleotide segid 14832.
 Pred. No. 1.3e-23;
0; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Screen SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 14832; 15pp; English.
                                                                                                                                                                                                                                               TGCCCAATTACAAGACCTT 230
                                                                                                                                                                                                                                                                          352 rccccacrarrecaccer 370
                                                                                                                                                                                                                                                                                                                                                             ADX32012 standard; cDNA; 704 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAY-1999; 99US-00304517.
                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein content; gene; ss.
Best Local Similarity 74.9
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KOVALIC D K.
SCREEN S E.
TABASKA J E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-180133/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
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(CAOY/)
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(SCRE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAAAGGCTTTTAGCTGTTTATGACAAGGACACTCCTGACCGTTGGTACAATGTTGCTCAT 269
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plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme semetic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifiying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCATCAACATCGAGACTGGTCGTGTCCCTTTGCCCAATTACAAGA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            330 GTTÁAGCATÁTTGÁGTCTGGACGTGTGCCATTCCCAAATTACAAGA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 704 BP; 202 A; 159 C; 121 G; 222 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADJ43786 standard; cDNA; 466 BP
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26-SEP-2001; 2001US-0325448P.
04-APR-2002; 2002US-0370620P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.1%;
68.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLAZEBROOK J.
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COOPER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GOFF S A.
KATAGIRI F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant cDNA #4786.
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                                                                                                                                                                                                                                                                                                                                                                                      nvention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOUG/)
(BRIG/)
(COOP/)
(GLAZ/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
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The invention relates to plant nucleotide sequences that direct seed, claff and/or stem-, panicle-, root- or pollen-specific or -preferential or constitutive transcription of an operatively linked nucleic acid segment. The invention also relates to a method for augmenting a plant consecription of an enthod for augmenting a plant consecription is a cereal, pollen, root or is constitutive in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower, canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley, concode are useful for manipulating crop plants to alter or improve proteins, to incur resistance to insecticides, viruses or fungi, and to proteins, to incur resistance to insecticides, viruses or fungi, and to proteins, to incur resistance to insecticides, viruses or fungi, and to incur stress tolerance (e.g. salt, cold or drought) to ensure the plants have a high nutritional value with reduced apical dominance or dwarfism, early flowering or altered metabolic pathways. This sequence represents a plant with an expension of the invention, or early flowering or altered metabolic pathways. This sequence represents a plant with a sequence date for this incur in the control or drought to a control or drought.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAGTGAAGCGGCACTACGAGCTGCTGGTGGCGGACATTATCCTCATCGAGAAGGGCCAG 228
                                                                                                                                                                                rice promoter, useful for manipulating crop plants to alter or
prove phenotypic characteristics, e.g. produce large quantities of oil
proteins, resistance to insecticides, virus or fungi, stress tolerance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at segdata.uspto.gov/seguence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGGACACACCCGACCGATGCCACAATGTGGCAAAAGCTGTCGGAGGGAAAACTGTAGAA 144
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                                                                                        r B, Glazebrook Ricke D, Zhu T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Argectrosagechartraccecrectedecenerageserrenda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 110; DB 12;
Pred. No. 3.8e-21;
                                                                                            s SP, Cooper
Provart N, R
                                                                                                                                                                                                                                                                                   Example 13; SEQ ID NO 4786; 230pp; English.
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                                                                                            Briggs SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                              Kreps J,
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                                                                                                                                                                                                                                               high nutritional value.
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                                                                                            P, Moughamer
Katagiri F,
                                                                                                                                                     WPI; 2004-190374/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
KREPS J.
PROVART N.
RICKE D.
                                                          ZHU T.
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                                                                                              Budworth P,
                                                                                                                                                                                          New rice I
improve pl
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                                                                                                               Goff SA,
                   (PROV/)
(RICK/)
                                                          (ZHUT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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990S-0128714P
990S-0130449P
990S-0130449P
990S-0130489P
990S-0131449P
990S-0131449P
990S-0132484P
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                                                  Arabidopsis thaliana
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01-APR-1999;
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08-APR-1999;
16-APR-1999;
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     and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the stress, osmotic stress or any of their combinations. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                     New stress-responsive nucleic acid, useful for altering the responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold stress, salt stress or osmotic stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       476 crccrccrdeacceceaageagaacaacaacarcrccaagaagecacreecegreraceacag 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         416 GGACACCCCGGACGCCTCGCACAGATCGCCCGGGCCATCGGCGGGAAGACGGCGGACGA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel abiotic stress responsive polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 CTCACCATGGACGTTTAGTCAAACAAGATGTTCGAGAGGGCCTTGGCAGTTTACGACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 513 BP; 126 A; 128 C; 127 G; 131 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 9482; 89pp; English
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N, Ricke D,
                                                                                                                                                (SYGN ) SYNGENTA PARTICIPATIONS AG.
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                                                          21-JUN-2002; 2002WO-US019668
                                                                                   22-JUN-2001; 2001US-0300112P
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26-SEP-2001; 2001US-0325277P
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Moughamer T, Provart
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           WO2003008540-A2
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GAGAGGCCTTGGCAGTTTACGACAAGGACACCCGACCGATGGCACAATGTGGCAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
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Pred. No. 1.1e-20;
0; Mismatches 71
99US-0151930P.
99US-0152163P.
99US-0153758P.
99US-0154779P.
99US-015413P.
99US-015413P.
99US-015542P.
99US-0155659P.
99US-0156659P.
99US-0156658P.
99US-015663P.
99US-0157117P.
99US-015713P.
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68.0%;
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Best Local Similarity
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Gaps

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ACNS9055 standard; cDNA; 577

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ACN59055

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129 AGGGAAAACTGTAGAAGAAGTGAAGCGCCACTATGACATTCTCGTCGAGGATCTCATCAA 188 AGAGAAAACTGTTGAGGAAGTGAAGAAGCACTATGAGCTTCTTCTTGAAGATGTTAGACG 268

CATCGAGTCGGGTCGCGTTCCTTTCCCCGACTATTGGACCGT 310 CATCGAGACTGGTCGTGCCCTTTGCCCCAATTACAAGACCTT

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ACN61224 standard; cDNA; 505

ACN61224/c

ACN61224;

02-DEC-2004 (first entry)

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89 AATGICATCGATTICAATGICTGGTTCATGGACAGCCAACAAACAAAGATTCGAAGGGC CTTGGCAGTTTACGACAAGGACACCCGACCGATGGCACAATGTGGCAAAAGCTGTCGG

**AAACTCAAGAAGTTCAATCTCACCATGGACGTTTAGTCAAAACAAGATGTTCGAGAGGGC** 

(first entry)

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The invention relates to 17880 cotton expressed sequence tags (ESTS;

ACN45220-ACN63099). The ESTS were isolated from CDNA libraries generated
from primed or non-primed seeds from variety DPSOB, mature seeds from
variety Coker 112 Boswell 96 Field, and androecium tissue, gynoecium
tissue, developing fibres, carpel walls and septa from variety
CC transformed seeds from valiety procing
CC seed for the invention also relates to substantially purified
proteins or their fragments encoded by nucleic acid molecules of the
invention, and to transformed plants having a nucleic acid construct
CC comprising a nucleic acid of the invention. The cotton ESTS are useful as
molecular tags to isolate genetic regions, to isolate genes to meders, to determine gene function and to determining whether genes are
CC determine gene function and to determining whether genes are
CC seed for isolate genetic regions, to isolate genes are
CC seed for isolate gene family. The nucleic acid molecules may be
used for isolating a variety of agronomically significant genes
cc associated with plant growth, quality, yield, and could also serve as
Inks in metabolic and catabolic pathways. The nucleic acid molecules are
clinks in metabolic and catabolic pathways. The nucleic acid molecules
cc associated with plant growth, quality, yield, and could also serve as
clinks in metabolic and catabolic pathways. The nucleic acid molecules
cc associated with plant growth, quality, yield, and could also serve as
clinks in metabolic and catabolic pathways and could also serve as
cc agronomically significant genes important in initiating and maintaining
cs edd germination or that may be used to mitigate stresses encountered
cc during seed germination. The ESTs additionally enable the acquisition of
cs promoters and cis-regulatory elements which will be useful for
cc detecting the expression level or pattern of a protein or mRNA and for
detecting the expression level or pattern of a protein or mRNA and for
cc detecting the expression level or pattern of a protei
                                                                                                 Cotton; plant; EST; expressed sequence tag; transgenic plant; gynoecium; variety Nucotton;38; library LIBSR2; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular
Cotton gynoecium tissue EST Clone ID: LIB3829-015-Q1-K6-E2, SEQ:13836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            patent office at segdata.uspto.gov/sequence.html?DocID=US20040123340
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FENG P C C.
FINCHER K L.
ZIEGLER T E.
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(FINC/)
(ZIEG/)
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Cotton; plant; EST; expressed sequence tag; transgenic plant; gynoecium; variety Nucottoni38; library LISB3829; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; se.

Gossypium hirsutum.

US2004123340-A1. 24-JUN-2004.

Cotton gynoecium tissue EST Clone ID: LIB3829-034-Q1-N6-A10, SEQ:16005.

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ACW45220-ACN63099). The ESTS were isolated from cDNA libraries generated from primed or non-primed seeds from variety DPSOB, mature seeds from variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium tissue, developing fibres, carpel walls and septe from variety Nucotton33B. The invention also relates to substantially purified proteins or their fragments encoded by nucleic acid molecules of the invention, and to transformed plants having a nucleic acid construct comprising a nucleic acid of the invention. The cotton ESTs are useful as molecular tags to isolate genetic regions, to isolate genes, to map genes, to determine gene function and to determining whether genes are members of a particular gene family. The nucleic acid molecules may be used for isolating a variety of agronomically significant genes as associated with plant growth, quality, yield, and could also serve as links in metabolic and catabolic pathways. The nucleic acid molecules are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to 17880 cotton expressed sequence tags (ESTs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ziegler TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 16005; 34pp; English.
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                                                                                                                                                                                                                                                                                                                                 12-DEC-2001; 2001US-00021323.
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(FENG/) FENG P C C.
(FINC/) FINCHER K L.
(ZIEG/) ZIEGLER T E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-479808/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tags to map genes.
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Gaps

28.5%; Score 108:4; DB 13; Length 577; 68.0%; Pred. No. 1.2e-20; ive 0; Mismatches 71; Indels 0;

Best Local Similarity 68.0 Matches 151; Conservative

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGGAAGTGAAGTTGCATTACCAGAACCTTGTGGATGACATCAAGCAGATAGAGTCTGGG 287
also useful for identifying genes important in initiating and maintaining dering that may be used to mitigate stresses encountered during seed germination. The ESTs additionally enable the acquisition of promoters and cis-regulatory elements which will be useful to express addronomically significant genes in these tissues and/or other tissues, and also permits the acquisition of molecular markers useful in breeding schemes, genetic and molecular mapping, and in cloning of agronomically significant genes in these tissues and/or other tissues, significant genes. The nucleic acid molecular apping, and in cloning of agronomically significant genes. The nucleic acid molecules are further useful for detecting the presence or quantity of a protein or mRNA and for detecting the presence or quantity of a protein by tissue printing. The present sequence represents a specifically claimed EST isolated from a sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed from the US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 TCAATCTCACCATGGACGTTTAGTCAAAACAAGATGTTCGAGAGGGCCTTGGCAGTTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACAAGGATACACCAGACCGGTGGCACAAGCTAGCCAGGGCTGTTGGGGGGGAAGACCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGAAGTGAAGCGCCACTATGACATTCTCGTCGAGGATCTCATCAACATCGAGACTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                               patent office at segdata.uspto.gov/sequence.html?DocID=US20040123340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.2%; Score 107.4; DB 13; Length 505; 70.2%; Pred. No. 2.2e-20; rive 0; Mismatches 61; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 505 BP; 131 A; 114 C; 102 G; 158 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGTGTCCCTTTGCCCAATTACAAGA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 10.4
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   466
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Cotton; plant; EST; expressed sequence tag; transgenic plant; gynoecium; variety Nucotton33B; library LIB3829; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.
                                                                              Cotton gynoecium tissue EST Clone ID: LIB3829-034-Q1-K6-A10, SEQ:14482.
                   BP.
                   ACN59701 standard; cDNA; 532
                                                           (first entry)
                                                           02-DEC-2004
                                       ACN59701;
RESULT 15
          ACN59701
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CACGTGCCTTTGCCCCTTACAAGA 262

286

유

Gossypium hirsutum US2004123340-A1. 24-JUN-2004. Search completed: March 10, 2006, 18:43:29 Job time : 404 secs

Ziegler TE;

Fincher KL,

Feng PCC,

<del>ب</del>

Deikman

WPI; 2004-479808/45.

14-DEC-2000; 2000US-025519P.

(DEIK/) DEIKMAN J. (FENG/) FENG P C C. (FINC/) FINCHER K L. (ZIEG/) ZIEGLER T E.

12-DEC-2001; 2001US-00021323

caccircriricccccriricaaca 260

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The invention relates to 17880 cotton expressed sequence tags (ESTS;
ACNA5220-ACN63099). The ESTS were isolated from CDNA libraries generated
CC from primed or non-primed seeds from variety DPSOB, mature seeds from
variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
tissue, developing fibres, carpel walls and septa from variety
CC tissue, developing fibres, carpel walls and septa from variety
Nucotton33B. The invention also relates to substantially purified
comprising a nucleic acid of the invention. The cotton ESTs are useful as
comprising a nucleic acid of the invention. The cotton ESTs are useful as
comprising a nucleic acid of the invention. The cotton ESTs are useful as
comprising a nucleic acid of the invention. The cotton ESTs are useful
comprising a nucleic acid of the invention. The cotton ESTs are useful
comprising a nucleic acid of the invention, to isolate genes to members of a particular gene family. The nucleic acid molecules may be
comprising an estabolic and catabolic pathways. The nucleic acid molecules are
associated with plant growth, quality, yield, and could also serve as
clinks in metabolic and catabolic pathways. The nucleic acid molecules are
compressed germination or that may be used to mitigate stresses encountered
consected germination or that may be used to mitigate stresses encountered
consecting seed germination. The ESTs additionally enable the acquisition of
promoters and cis-regulatory elements which will be useful to expressing
consecting the acquisition of molecular markers useful for
cotton variety Nucotton318 gynoecium tissue control or mRNA and for
detecting the expression level or pattern of a protein or mRNA and for
detecting the expression level or pattern of a protein or mRNA and control and control variety Nucotton318 gynoecium tissue control or providence data for this patent did not forme to the printed
cotton variety Nucotton318 gynoecium tissue control or providence data for this patent did not forme to the printing or present expression level or p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAATCTCACCATGGACGTTTAGTCAAAACAAGATGTTCGAGAGGGCCTTGGCAGTTTAC 81
New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 GACAAGGACACACCCGACCGATGGCACAATGTGGCAAAAGCTGTCGGAGGGAAAACTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               patent office at segdata.uspto.gov/sequence.html?DocID=US20040123340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 107.4; DB 1:
Pred. No. 2.2e-20;
0; Mismatches 61
                                                                                                                                       Claim 1; SEQ ID NO 14482; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGTGTCCCTTTGCCCAATTACAAGA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 144; Conservative
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                                                                                        tags to map genes.
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-MODEL=frame+ p2n.model -DEV=xlp
-MODEL=frame+ p2n.model -DEV=xlp
-Q=/abss/ABSWEB spool/US1069778/Tunat_09032006 150641_3661/app_query.fasta_1
-D=Published Applications NA New -OFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bIts -START=1 -END=-1 -MATRIX=blosum62
-TRANS=humand, 0.di -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSTZE=500 -MINLEN=0
-WAXIEN=200000000 -HOST=abss05p
-USREAUS10697787 @CGM 1 1 653 @runat 09032006 150641_3661 NCPU=6 -ICPU=3
-NO MMAP -NEG_SCORES=0 -MAIT -DSPBLOCK=100 -LÖNGLOG -DEV_TIMEOUT=120
-NARN_TIMEOUT=30 -THRRADS=1 -XGAPPOP=10 -XGAPEXT=0.5 -FGAPFOR=7
-YGAPEXT=0.5 -DBLOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8355, Ap
Sequence 4492, Ap
Sequence 245, App
Sequence 273, App
                                                                                                                                       March 10, 2006, 19:35:45 ; Search time 442 Seconds (without alignments) 657.736 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                      US-10-697-787-2
656
1 MASNSRSSISPWTFSQNKMF......HSSDFEKFSQKVLVSYISLV
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1: /cgn2_6/ptodate/2/pubpna/US06_NEW_PUB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                         nucleic search, using frame_plus_p2n model
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US-11-096-568A-4492
US-10-714-887-245
US-10-714-887-273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7673375 seqs, 1153648444 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                    0.5
7.0
7.0
                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
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1724
866
896
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32.6
32.2
31.1
                                                                                                                                                                                                                                      Title:
Perfect score:
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214
211
204
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                                                                                            OM protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
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                                                                                                                                            Run on:
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        5
        193
        29.4
        957
        9 US-11-086-568A-21919
        Sequence 102, App

        186.7
        28.5
        876
        9 US-11-086-568A-21894
        Sequence 2366, A

        146
        23.1
        1954
        9 US-11-096-568A-12894
        Sequence 21864, A

        11
        146
        22.3
        1951
        9 US-11-096-568A-12836
        Sequence 21864, A

        11
        124
        18.9
        9 US-11-096-568A-12836
        Sequence 21864, A

        12
        18.4
        600
        12 US-11.136-527-414
        Sequence 24021, A

        12
        18.4
        600
        12 US-11.136-527-414
        Sequence 24021, A

        18
        18.5
        18.7
        60
        18.51-11.136-527-414
        Sequence 24021, A

        18
        18.5
        18.7
        60
        18.50-11.136-527-618
        Sequence 2102, A

        18
        18.5
        18.7
        60
        18.50-11.136-527-618
        Sequence 20638, A

        18
        18.5
        18.7
        60
        18.50-11.136-11.136-11.136
        Sequence 20638, A

        18
        18.5
        18.7
        18.5
        18.5
        18.5
        18.5

        18
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## LIGNMENT

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RESULT 1

US-11-096-568A-8355

Sequence 8355, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Ther
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OTHER INFORMATION: G2701 reference sequence; predicted polypeptide sequence is para
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APPLICANT: AFFLICANT: AFFLIATES, ROGER
APPLICANT: KURNET, ROGERICK W
APPLICANT: KURNET, Peter
APPLICANT: KURNET, Lynne
APPLICANT: REBER, T. Lynne
APPLICANT: REBER, T. Lynne
APPLICANT: REBER, T. Lynne
APPLICANT: REBER, T. Lynne
APPLICANT: BISTOSS-CIP
CURRENT PILING DATE: 2003-04-10
FILE REFERENCE: MURBER: 10/412,699
FRIOR PILING DATE: 2003-04-10
FRIOR PAPLICATION NUMBER: 09/506,720
FRIOR PAPLICATION NUMBER: 09/506,720
FRIOR APPLICATION NUMBER: 09/506,720
FRIOR APPLICATION NUMBER: 09/533,392
FRIOR APPLICATION NUMBER: 09/533,392
FRIOR PILING DATE: 1999-09-13
FRIOR PILING DATE: 2000-03-22
FRIOR APPLICATION NUMBER: 09/533,039
FRIOR PILING DATE: 2000-03-22
FRIOR PELING DATE: 2000-03-22
FRIOR APPLICATION NUMBER: 09/533,030
FRIOR PILING DATE: 2000-03-22
FRIOR PELING DATE: 2000-03-23
FRIOR PELING DATE: 2000-03-23
FRIOR PELING DATE: 20
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                                                                                                                                                                                                           APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: HEARD, Jacqueline
APPLICANT: RIECHMANN, Jose Luis
APPLICANT: CREELMAN, ROBER
APPLICANT: RATCLIFFE, Oliver
                                                                                                                                     Sequence 245, Application US/10714887; Publication No. US20060015972A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Arabidopsis thaliana
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Best Local Similarity:
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LENGTH: 866
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Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICANT: Alexandrov, Nickolai et al.
TAPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-15922US2
CURRENT APPLICATION US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 SerIleAsnAspPheAspThrArgTyrIleThrLysTyrLeuTyrMetMetLeuSerIle 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 GlyGlyLysThrValGluGluValLysArgHisTyrAspIleLeuValGluAspLeuIle 62
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                                                                                                               SerAsnSerArgSerSerIleSerProTrpThrPheSerGlnAsnLysMetPheGluArg 22
                                                                                                                                                                 GCTACAACAATGGCCTCAAGTCAGGGTTGGACTCCGAAGCAGGAACAAGAGATTTGAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                      63 AsnileGluThrGlyArgValProLeuProAsnTyrLysThrPheGluSerAsnSerArg
                                                                                                                                                                                                                           AlaLeuAlaValTyrAspLysAspThrProAspArgTrpHisAsnValAlaLysAlaVal
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                                                               US-10-697-787-2 (1-126) x US-11-096-568A-8355 (1-517)
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COTHER INFORMATION: Ceres Seq. ID no. 13638441
US-11-096-568A-4492
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354 ATTTAT 359
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*US-11-096-568A-29719

; Sequence 29719, Application US/11096568A

; Sequence 29719, Application US/20060048240A1

; GENERAL INFORMATION:

; APPLICANT: Alexandrov, Nickolai et al.

; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide

; TITLE OF INVENTION: Therby

; FILE REFERENCE: 2750-1592PUS2
                                                                        166 GACACGCCTGATCGCTGCTTCAAAGTTGCTGCTATGATCCCTGGAAAGACCATATCAGAT 225
                                                                                                                                                                            109 ridakciagagarakadakaagriridaaagricccricciararardadagacacc 168
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                                 30 AspThrProAspArgTrpHisAsnValAlaLysAlaValGlyGlyLysThrValGluGlu 49
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                                                                                                                                          ValLysArgHisTyrAspIleLeuValGluAspLeuIleAsnIleGluThrGlyArgVal
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                                                                                                                                                                                                                                                                                                                                                                            'Sequence 102, Application US/11087099
'Sequence 102, Application US/11087099
'PUblication No. US20060041961A1
'GENERAL INFORMATION:
'APPLICANT: Abad, Mark S. et al.
'TITLE OF INVENTION: Genes and Uses for Plant Improvement
'FITE REFERENCE: 38-21(53450)B EP
'CURRENT APPLICATION NUMBER: US/11/087,099
'CURRENT FILING DATE: 2005-03-22
'NUMBER OF SEQ ID NOS: 12464
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LENGTH: 957
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                                               229 ATGATCCCTGGAAGACTGTTTTTGATGTTATGAAGCAATATAGTAAGCTTGAAGAAGAC 288
41 AlavalGlyGlyLysThrValGluGluValLysArgHisTyrAspIleLeuValGluAsp 60
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                                                                                                                                     GITTICGAIATIGAAGCAGGACGIGITTCCCCAITATCCTGCAGCTICTTCT 345
                                                                                                    61 LeulleAsnileGluThrGlyArgValProLeuProAsnTyrLysThrPheGluSer 79
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Publication No. US20060015972A1
GENERAL INFORMATION:
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Best Local Similarity:
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US-10-714-887-273
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US-11-096-568A-23894

Sequence 23894, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:

TITLE OF INVENTION: Therby

TITLE OF INVENTION: Therby

FILE REFERENCE: 2750-1592PUS2

CURRENT ALPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 23894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20386, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
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                                                                                                                             271 GACGCGAGGTGGGAGAAGCTAGCGGAGGCCGTCGAGGGAAGACGCCGGAGGTCAGG 330
                                                                                                                                                                                                     264 CCCGACAGGTGGGAGAAGGTGGCGGGGGGGGGCTGCCTGGAAGACGGTCGACGACGACGACGTGAGG 323
 151 ATGGCCGTGAACGAGGCGAGCAGCAGTGGCGGTGGGGAGGAGGAGGGGGTGCGGGTCGTGGACC 210
                                   14 PheSerGlnAsnLysMetPheGluArgAlaLeuAlaValTyr-----AspLysAspThr 31
                                                                                                           32 ProAspArgTrpHisAsnValAlaLysAlaValGlyGlyLysThrValGluGluValLys 51
                                                                                                                                                                              52 ArgHisTyrAspIleLeuValGluAspLeulleAsnIleGluThrGlyArgValProLeu 71
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Matches:
Conservative:
Mismatches:
Indels:
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... OTHER INFORMATION: Ceres Seq. ID no. 12416292
US-11-096-568A-23894
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ORGANISM: Zea mays subsp. mays
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151.50
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Best Local Similarity:
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US-11-096-568A-21266
Sequence 21266, Application US/11096568A
Sequence 21266, Application No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrow, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: 10-1592PUSC
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 21266
LENGTH: 1254
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Matches:
Conservative:
Mismatches:
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Mismatches:
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; OTHER INFORMATION: Ceres Seq. ID no. 12402516
US-11-096-568A-21266
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Matches:
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CURRENT APPLICATION NUMBER: US/11/096,568A CURRENT FILING DATE: 2005-04-01 NUMBER OF SEQ ID NOS: 34471 SEQ ID NO 29719 LENGTH: 876
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                                                                                                 TYPE: DNA
ORGANISM: Arabidopsis thaliana
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LOCATION: (1) ..(876)
CTHER INFORMATION: Ceres Seq.
US-11-096-568A-29719
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide TITLE OF INVENTION: Therby FILE REFERENCE: 2750-1592PUS2 CURRENT APPLICATION NUMBER: US/11/096,568A CURRENT FILING DATE: 2005-04-01 NUMBER OF SEQ ID NOS: 34471 SEQ ID NO 24021 LENGTH: 933
                                                                                                                                                                                                                                                         274 TGGACACGGGAGGAGGAGGAGGTTCGAAGAACGCGGTGGCGGCCGCCGCCGCCGCCGCC 333
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             Matches:
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LOCATION: (1). (933)
OTHER INFORMATION: Ceres Seq. ID
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55.8%
40.3%
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                     Percent Similarity:
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Best Local Similarity:
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US-11-096-568A-24021
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Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REPERBNCE: 2750-1592P0S2
CURRENT PILLING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 13836
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TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592FUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 20386
LENGTH: 1351
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; LOCATION: (1)..(1351)
; OTHER INFORMATION: Ceres Seq. ID
US-11-096-568A-20386
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NAME/KEY: misc feature
LOCATION: (901)
COTHER INFORMATION: n is a, c, t, US-11-096-568A-13836
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                                                                                                                                                                             TYPE: DNA
ORGANISM: Zea mays subsp. mays
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LOCATION: (1). (1431)
OTHER INFORMATION: Ceres Seq.
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Best Local Similarity:
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Publication No. US20050287570A1

GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wyeth
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR APPLICATION UNDER: 2005-06-26
NUMBER OF SEQ ID NOS: 352830
SSOTHARE: Patentin version 3.2
LENGTH: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                      11 ProTrpThrPheSerGlnAsnLysMetPheGluArgAlaLeuAlaValTyrAspLysAsp 30
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APPLICANT: Wyeth
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR PELING DATE: 2005-05-05
NUMBER OF SEQ ID NOS: 362830
SSCTWARE: Patentin version 3.2
SEQ ID NO 618
LENGTH: 2119
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US-11-136-527-4714
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; ORGANISM: Rattus norvegicus
US-11-136-527-618
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                                                                         ThrproAspargTrpHisAsnValAlaLysAlaValGlyGlyLysThrValGluGluVal
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APPLICANT: KERR, Richard
APPLICANT: ROSENELD, David
APPLICANT: ROSENELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMIL100-2
CURRENT APPLICATION UNDBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
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Matches:
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Mismatches:
Indels:
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PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 30681
LENGTH: 1593
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; Sequence 30681, Application US/10750185
; Publication No. US20050260603A1
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ORGANISM: Bovine 19866881746860
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1293 CAAACACTAGAAATG 1279
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APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
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US-10-750-623-30681/c

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16 GlnAsnLysMetPheGluArgAlaLeuAlaValTyrAspLysAspThrProAspArgTrp 35
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Sequence 306910.4 Application US/10750623
FUDLication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MAI GENOMICS, INC.
APPLICANT: DANISE, Sue K.
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: MAITHOR AND SYSTEMS FOR INFERRING BOVINE TRAITS
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
TITLE OF INVENTION WUMBER: US/10/750,623
CURRENT APPLICATION NUMBER: US 60/437,482
FRICR APPLICATION NUMBER: US 60/437,482
FRICR APPLICATION NUMBER: US 60/437,482
FRICR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PALENTIN VERSION 3.1
ENGTHARE: PALENTIN VERSION 3.1
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Job time : 445 secs
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; ORGANISM: Bovine 19866881746860
US-10-750-623-30681
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## Sequence 1, Application US/10697787

## Sequence 1, Application US/10697787

## Publication No. US20040216182A1

## Publication No. US20040216182A1

## Publication No. US2004021618A1

## Publication No. US2004021618A1

## APPLICANT: Agrinomics, LLC

## TITLE OF INVENTION: Generation of Plants with Improved Pathogen Resistance and

## TITLE OF INVENTION: Generation of Plants with Improved Pathogen Resistance and

## TITLE OF INVENTION: Generation Of Plants AG03-071C

## CURRENT APPLICATION NUMBER: US/10/697,787

## PRIOR PILING DATE: 2002-04-24

## PRIOR PILING DATE: 2003-04-24

## PRIOR PILING DATE: 2003-04-24

## NUMBER OF SEQ ID NOS: 18

## SOFTMARE: PatentIn Version 3.2

## LENGTH: 301

** LENGTH: 301
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US-10-697-787-18

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US-10-260-238-4786

US-10-261-328-4786

US-10-767-795-271

US-10-424-599-5904

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US-10-424-599-5904

US-10-021-323-14482

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US-10-021-323-14482

US-10-021-323-14482

US-10-1323-1482

US-10-21-323-1483

US-10-254-403-63

US-10-425-115-16525

US-10-425-115-16525

US-10-425-115-16525

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ORGANISM: Arabidopsis thaliana
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Sequence 1, Appli
Sequence 6644, Ap
Sequence 270, App
Sequence 14832, A
                                                                                                                                                           March 10, 2006, 19:35:01 ; Search time 657 Seconds (without alignments) 1585.908 Million cell updates/sec
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1: /cgn2 6/ptodata/1/pubpna/USO7 PUBCOMB.seq:*
2: /cgn2 6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
3: /cgn2 6/ptodata/1/pubpna/USO8A_PUBCOMB.seq:*
4: /cgn2 6/ptodata/1/pubpna/USO8B_PUBCOMB.seq:*
5: /cgn2 6/ptodata/1/pubpna/USLOB_PUBCOMB.seq:*
6: /cgn2 6/ptodata/1/pubpna/USLOB_PUBCOMB.seq:*
7: /cgn2 6/ptodata/1/pubpna/USLOB_PUBCOMB.seq:*
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9: /cgn2 6/ptodata/1/pubpna/USLOB_PUBCOMB.seq:*
10: /cgn2 6/ptodata/1/pubpna/USLOB_PUBCOMB.seq:*
                      GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                OM protein - nucleic search, using frame_plus_p2n model
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US-10-512-600-1
US-10-424-599-6644
US-10-767-795-270
US-10-425-114-14832
US-10-424-599-135729
US-09-770-152-473
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Database :

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Sequence 18, Appl Sequence 271, App Sequence 271, App Sequence 5904, Ap Sequence 9309, Ap Sequence 103390, Sequence 14482, A Sequence 14482, A Sequence 16005, A Sequence 16005, A Sequence 16525, Sequence 16525, Sequence 27843, Appl Sequence 27843, Appl Sequence 433, Appl Sequence 661, Appl Sequence 61, Appl Sequence 61, Appl Sequence 61, Appl Sequence 63, Appl Sequence 27843, Appl Sequence 27843, Appl Sequence 27899, A Sequence 27899, A Sequence 27899, A Sequence 26642, A Sequence 26642, A Sequence 5664, A Sequence 5670, Ap Sequence 5670, Ap Sequence 5670, Ap Sequence 5671, Ap

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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Exercise Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 6644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HisSerSerAspPheGluLysPheSerGlnLysValLeu---ValSerTyrIleSerLeu 125
                                                                                          AsniysMetPheGluArgAlaLeuAlaValTyrAspiyeAspThrProAspArgTrpHis 36
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Sequence 6644, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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; Sequence 1, Application US/10512600
; Publication No. US20050210546A1
; GENERAL INFORMATION:
APPLICANT: AGRINOMICS, LLC
; TITLE OF INVENTION: GENERALION OF PLANTS WITH IMPROVED PATHOGEN RESISTANCE
; FILE REFERENCE: AGO3-0330-US
; CURRENT APPLICATION NUMBER: US/10/512,600
; CURRENT FILING DATE: 2004-10-22
; PRIOR PILING DATE: 2004-10-22
; PRIOR PILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
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                                           21 GluArgAlaLeuAlaValTyrAspLysAspThrProAspArgTrpHisAsnValAlaLys
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                              MetAlaSerAsnSerArgSerSerIleSerProTrpThrPheSerGlnAsnLysMetPhe
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    US-10-697-787-2 (1-126) x US-10-697-787-1 (1-381)
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, OTHER INFORMATION: Clone ID: LIB3028-039-A6_FLI
US-10-425-114-14832
                                                                                        Percent Similarity:
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Publication No. US20040034888A1

GENERAL INPORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Screen, Secven E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Dance E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 14832
                                                                       Sequence 270, Application US/10767795
Publication No. US20040181830A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
CURRENT APPLICANTON: 38-21(53534)B
CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT FILING DATE: 2004-01-30
                    616
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1 MetAlaSerAsnSerArgSerSerIleSerProTrpThrPheSerGlnAsnLysMetPhe
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; OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C42883_2
US-10-767-795-270
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Matches:
Conservative:
Mismatches:
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290.00
83.8%
70.0%
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Best Local Similarity:
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US-10-425-114-14832
                                                             US-10-767-795-270
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LENGIH: 760
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: VOIGHTS and Uses Thereof for Plant Improvement
TITLE OF INVENTION: VOIGHTS and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 135729
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                                                                                                                                                                                                                                                                                                               210 GAAAAGGCTTTAGCTGTTTATGACAAGGACACTCCTGACCGTTGGTACAATGTTGCTCAT 269
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                                                                                                                                                                                                               41 AlaValGlyGlyLysThrValGluGluValLysArgHisTyrAspIleLeuValGluAsp
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 Oy 1 MetalaSerAsnSerArgSerSerIleSerProTrbThrP
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Indels:
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                                                                                                                                             US-10-697-787-2 (1-126) x US-10-425-114-14832 (1-704)
                                                                                                         Gaps:
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; Sequence 135729, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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287.00
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66.7%
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80.2%
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43.8%
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APPLICANT: FLIGANT: APPLICANT
APPLICANT: FLIGANT: APPLICANT: FLIGAND:
APPLICANT: REUBER, T. Lynne
APPLICANT: CREELMAN, Robert A
APPLICANT: CREELMAN, Robert A
APPLICANT: PROBER, T. Lynne
APPLICANT: YU, Guo-Liang
APPLICANT: YU, Guo-Liang
APPLICANT: YU, Guo-Liang
APPLICANT: YO, Suo-Liang
CURRENT APPLICANTION NUMBER: US/10/225,066A
CURRENT FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-12-11
PRIOR FILING DATE: 2001-03-13
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59 GluaspLeulleAsnileGluThrGlyArgValProLeuProAsnTyrLysThrPheGlu 78
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Sequence 359, Application US/10225066A

Sequence 359, Application US/10225066A

GENERAL INFORMATION:
APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: RATCLIFFE, Oliver
APPLICANT: ADAM. Luc 3
APPLICANT: DUBELL, ARROLd
APPLICANT: DUBELL, ARROLd
APPLICANT: PILGRIM, Marsha L
APPLICANT: PILGRIM, Marsha L
APPLICANT: PILGRIM, Marsha L
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity:
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LENGTH: 578
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APPLICANT: Slader, Ted
APPLICANT: Jane, Ted
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neith
APPLICANT: Hoffman, Neith
APPLICANT: Hoffman, Neith
APPLICANT: Hurban, Partick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: LAbilana
FILE REFERENCE: 2025US (PARA-014PRU)
CURRENT APPLICATION NUMBER: US/09/770,152
FURRENT APPLICATION NUMBER: 60/178,503
PRIOR FILING DATE: 2000-01-27
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Matches:
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                              RESULT 7
18.09-770-152-473/c
18.09-770-152-473/c
18.09-770-152-473/c
18.09-770-152-473/c
19.09-770-152-473/c
19.09-770-152-473
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Rameaka, Joshua G.
Page, Amy
Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
Garcia, Carlos A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Arabidopsis thaliana
US-09-770-152-473
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LENGTH: 556
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APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: RATCLIFFE, Oliver
APPLICANT: RATCLIFFE, Oliver
APPLICANT: RIECHMANN, Jose Luis
APPLICANT: DUBEL, Arnold T
APPLICANT: HEARD, Jacqueline E
APPLICANT: HEARD, Jacqueline E
APPLICANT: HEARD, Jacqueline E
APPLICANT: CREELMAN, Rebert
APPLICANT: CREELMAN, Robert A
APPLICANT: PINEDA, Ommaira
APPLICANT: PINEDA, Ommaira
APPLICANT: YU, Guo-Liang
APPLICANT: Williang
APPLICANT: Yu, Guo-Liang
APPLICANT: Williang
APPLICANT: Yu, Guo-Liang
APPLICANT: Williang
APPLICANT: 
168 GCCTTTGAGCGTGCTCTAGCAGTCTATGACCAAAGACACTCCGGACCGTTGGCACAATGTT 227
                                                                                                                                                                                                                                                                                         288 CGTGACATCGAAAGCATCGAGAATGGTCACGTGCCATTCCCTGACTACAAGACTACTACA 347
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                                                                                                       39 AlaLysAlaValGlyGlyLysThrValGluGluValLysArgHisTyrAspileLeuVal
                                                                                                                                                         108 ATGCCATCAGGCTCAATGTCTTCTTATGGCTCTGGCTCATGGACTGTTAAGCAGAACAAA
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CURRENT FILING DATE: 2002-08-09
PRIOR PAPLICATION NUMBER: 09/837,444
PRIOR FILING DATE: 2001-04-18
PRIOR PILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR APPLICATION NUMBER: 60/310,849
PRIOR APPLICATION NUMBER: 60/318,692
PRIOR APPLICATION NUMBER: 60/318,692
PRIOR PILING DATE: 2001-12-11
PRIOR PILING DATE: 2001-12-11
PRIOR PILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 1122
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 359, Application US/10225066A Publication No. US20050160493A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Arabidopsis thaliana
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286.00
74.7%
67.5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                       348 GGAAACAGC 356
                                                                                                                                                                                                                                                                                                                                                                                      79 SerAsnSer 81
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-225-066A-359
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Pred. No.:
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LENGTH: 578
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288 CGTGACATCGAAAGCATCGAGAATGGTCACGTGCCATTCCCTGACTACAAGACTACTACA 347
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APPLICANT: PIGGIAL, PIETEE E
APPLICANT: PIGGIAL, MARINA
APPLICANT: PINGAA OMABITA
APPLICANT: PINGAA OMABITA
APPLICANT: PINGAA OMABITA
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBL - 0047 CIP
CURRENT APPLICATION NUMBER: US/20/2-25
PRIOR APPLICATION NUMBER: US/310,847
PRIOR PELING DATE: 2001-04-18
PRIOR PPLING DATE: 2001-08-22
PRIOR PPLING DATE: 2001-08-22
PRIOR PLING DATE: 2001-11-19
PRIOR PPLICATION NUMBER: 09/334,455
PRIOR PPLICATION NUMBER: 00/336,049
PRIOR PPLICATION NUMBER: 60/336,049
PRIOR PPLICATION NUMBER: 10/225,066
PRIOR PPLING DATE: 2001-11-19
PRIOR PPLING DATE: 2002-06-14
PRIOR PPLING DATE: 2002-06-19
PRIOR PPLING DATE: 2002-06-19
PRIOR PPLING DATE: 2002-06-19
PRIOR PPLING DATE: 2002-08-09
PRIOR PLING DATE: 2002-08-09
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Mismatches:
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Matches:
                                                                                                                                                                                                                                                                        Sequence 2719, Application US/10374780A Publication No. US20040019927A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Heard, Jacqueline E
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ORGANISM: Arabidopsis thaliana
FEATURE:
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Ratcliffe, Oliver
Adam, Luc J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reuber, T. Lynne
Keddie, James
Broun, Pierre E
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US-10-374-780A-2719
                                                                                                                                    348 GGAAACAGC 356
                                                                79 SerAsnSer 81
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Best Local Similarity:
Query Match:
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               ---SerTyrileSer 124
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                                                                                                                                                                                                      APPLICANT: Briggs, Steven P.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
APPLICANT: Cooper, Bret
APPLICANT: Gazebonn A.
APPLICANT: Gaff, Stephen A.
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Ricke, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REPERENCE: 60111-NP
CURRENT FILING DATE: 2002-09-26
PRIOR PELING DATE: 2001-09-26
PRIOR PELING DATE: 2001-09-26
PRIOR PELING DATE: 2001-09-26
PRIOR PELING DATE: 2001-09-26
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 4786
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Matches:
Conservative:
Mismatches:
Indels:
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  111 PheGluLysPheSerGlnLysValLeuVal----
                                                                                                         RESULT 12
US-10-260-238-4786/C
is Sequence 4786, Application US/10260238
is Publication No. US20040016025A1
is GENERAL INFORMATION:
APPLICANT: Budworth, Paul R.
APPLICANT: Moughamer, Todd G.
APPLICANT: Cooper, Bret
APPLICANT: Gleschrock, Jane
APPLICANT: Goff, Stephen A.
APPLICANT: Ratagiri, Funiyaki
APPLICANT: Katagiri, Funiyaki
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60.0%
47.1%
42.1%
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US-10-260-238-4786
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Best Local Similarity:
Query Match:
DB:
                                                           Leu 125
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Publication No. US20040216182A1

GENERAL INPORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/697,787

CURRENT APPLICATION NUMBER: US/10.29

PRIOR FILING DATE: 2003-10-29

PRIOR FILING DATE: 2003-04-24

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PATENTION NUMBER: US/33/12981

PRIOR FILING DATE: 2003-04-24

NUMBER OF SEQ ID NOS: 18

SEQ ID NO 18

LENGTH: 732
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                  ---LygThrPheGluSerAsnSerArgSerIleAsnAspPheAspThr-----Arg 90
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Matches:
Conservative:
Mismatches:
Indels:
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278.00
54.7%
42.9%
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US-10-697-787-18
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Best Local Similarity:
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Pred. No.:
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ORGANISM: Gossypium hirsutum
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Query Match:
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Best Local Similarity:
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                                                                                                               Alignment Scores:
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LENGTH: 507
                                        FEATURE:
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Publication No. US20040181830A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Shou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53534)B
CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT PILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 117596
                                                                                                                                                                                     APPLICANT: Deikman, Jill
APPLICANT: Peng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With FILE REPERENCE: 38-21(52274)8
FULE REPERENCE: 38-21(52274)8
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 16167
LENGHIS 543
                                     SerSerAspPheGluLysPheSerGlnLysValleu---ValSerTyrIleSerLeuVal 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 ileGluThrGlyArgValProLeuProAsnTyrLysThrPheGluSerAsnSerArgSer 83
                                                         7 SerSerIleSer-----ProTrpThrPheSerGlnAsnLysMetPheGluArgAla
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 132 CAATTACAAGAAACAGATACATACATATATGTGATG----
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Matches:
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                                                                                                                                         ; Sequence 16167, Application US/10021323; Publication No. US20040123340A1; GENERAL INFORMATION:
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ORGANISM: Gossypium hirsutum
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Best Local Similarity:
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LENGTH: 779
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Sequence 5904, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao vinds
APPLICANT: Cao 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 GAGAAAACTGTTGAGGAAGTGAAGAAGCACTATGAGGTTCTTCTTGAAGATGTTAGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 IleGluThrGlyArgValProLeuProAsnTyrLysThrPheGluSerAsnSerArgSer
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; OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C42883_1
US-10-767-795-271
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Matches:
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Sequence 1824, Ap Sequence 31207, A Sequence 14937, A Sequence 10919, A Sequence 2026, Ap Sequence 120, App Sequence 120, Appli Sequence 1, Appli

Sequence 1, Appli Sequence 2104, Appli Sequence 2104, App Sequence 1108, Ap Sequence 1486, App Sequence 1, Appli Sequence 1, Appli Sequence 1552, Ap Sequence 1552, Ap Sequence 1552, App Sequence 1152, App Sequence 1196, Appli Sequence 213, Appli Sequence 213, Appli Sequence 213, Appli Sequence 213, Appli Sequence 21460, Appli Sequence 214, Appli Sequence 23, Appli Sequence 24, Appli Sequence 27, Appli Sequence 21, Appli Sequence 11, Appli Sequence 11, Appli

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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Sequence 1581, Application US/09640211A

Sequence 1581, Application US/09640211A

Patent No. 683446

GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Glenn, Matchew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Composition of Gene Transcription
FILE REFRENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT APPLICATION NUMBER: US/09/640,211A

CURRENT FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 2368

SOFTARRE: PASESEQ for Windows Version 4.0

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US-09-640-211A-1824

US-09-270-767-31207

US-09-270-767-10919

US-09-640-211A-2026

US-09-640-211A-2026

US-09-640-211A-2026

US-09-640-211A-210

US-09-640-211A-2104

US-09-640-211A-2104

US-09-640-211A-2104

US-09-640-211A-2104

US-09-640-211A-1108

US-09-640-211A-1486

US-09-640-211A-1486

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US-09-350-729A-1
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US-09-640-211A-1581
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Sequence 1534, Ap
Sequence 1310, Ap
Sequence 20, Appl
Sequence 5801, Ap
Sequence 17541, A
Sequence 17541, A
Sequence 17541, A
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1 MASNSRSSISPWTFSQNKMF.......HSSDFEKFSQKVLVSYISLV
                     GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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                                                                                                         OM protein - nucleic search, using frame_plus_p2n model
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US-09-640-211A-1534
US-09-640-211A-1310
US-09-640-211A-1284
US-09-919-497-50
US-09-949-016-5801
US-09-949-016-17543
US-09-949-016-17543
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Maximum Match 100%
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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Sequence 11, Sequence 3, 3 SerAsnSerArgSerSerIleSerProTrpThrPheSerGlnAsnLysMetPheGluArg 22

US-10-697-787-2 (1-126) x US-09-640-211A-1581 (1-357)

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US-09-640-211A-1284

US-09-640-211A-1284

Sequence 1224, Application US/09640211A

Patent No. 683346

GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Sheath, Michael A.
APPLICANT: Glenn, Matchew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021GUU
CURRENT APPLICANTON NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368

SOFTWARE: FeatSEQ for Windows Version 4.0

LENGTH: 532
  Modification of Gene Transcription
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Matches:
Conservative:
Mismatches:
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Matches:
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                      FILE REFERENCE: 11000.1021CU
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1310
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ORGANISM: Eucalyptus grandis
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ORGANISM: Eucalyptus grandis
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25.3%
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Best Local Similarity:
     OF INVENTION:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                   43 GlyGlyLysThrValGluGluValLysArgHisTyrAspIleLeuValGluAspLeuIle 62
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                                                                                                                                                                                                                                                                                                                                                                 256 TGTATTGAAGCTGC-CGCGTTGCCCTACCCACGTAC------AGTAACTCT 299
                                                                                   AlaLeuAlaValTyrAspLysAspThrProAspArgTrpHisAsnValAlaLysAlaVal
                                                                                                                                                                                                                                                                                                             63 AsnileGluThrGlyArgValProLeuProAsnTyrLysThrPheGluSerAsnSer 81
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Sequence 1534, Application US/09640211A

Fatent No. 6833446

GENERAL INFORMATION:
APPLICANT: Shenk, Marian
APPLICANT: Shenk, Michael A.
APPLICANT: Glenn, Matchew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: Pates for Windows Version 4.0
SEQ ID NO 1534
LENGTH: 574
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Patent No. 6933446
GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Glenn, Matthew
ITILE OF INVENTION: Compositions and Methods for the
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Matches:
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66.7%
50.0%
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US-09-640-211A-1534
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Best Local Similarity:
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Query Match:
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ORGANISM: Human
JS-09-949-016-5801
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; ORGANISM: Human
US-09-949-016-17541
                                               Alignment Scores:
Pred. No.:
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Patent No. 681239

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUWAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PLILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 5801

LENGTH: 2069

LENGTH: 2069

LENGTH: 2069
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            52 ArgHisTyrAspIleLeuValGluAspLeuIleAsnIleGluThrGlyArgValProLeu 71
                                                                                                        348 ccaactraccaccaccaccaccaccaccaccaccacatraccrrrcaacaccaa 404
                                                                                                                                                                  Sequence 50, Application US/09919497;
Patent No. 6773883
GENERAL INFORMATION:
APPLICANT: MILTER, George L.
TITLE OF INVENTION:
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR PILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin version 3.0
SEQ ID NO 50
LENGTH: 1860
                                                                           ProAsnTyrLysThrPheGluSerAsnSerArgSerIleAsnAspPheAspThrArg
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Matches:
Conservative:
Mismatches:
Indels:
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124.00
64.2%
39.6%
18.9%
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US-09-919-497-50
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Best Local Similarity:
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US-09-949-016-5801
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Pred. No.:
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US-09-949-016-17541/c

1 Sequence 17541, Application US/09949016

1 Sequence 17541, Application US/09949016

1 Releant No. Gel12339

1 GENERAL INFORMATION:

2 APPLICANT: VEWTER, J. Craig et al.

1 TILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

1 TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

1 TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

1 CURRENT FILING DATE: 2000-04-14

2 PRIOR FILING DATE: 2000-10-20

3 PRIOR PELING DATE: 2000-10-03

3 PRIOR PELING DATE: 2000-10-03

4 PRIOR PILING DATE: 2000-10-03

5 PRIOR PILING DATE: 2000-09-08

6 NUMBER OF SEQ ID NOS: 207012

7 SOFTHARE: PERSECE for Windows Version 4.0

7 SEQ ID NO 17541
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  Length:
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34029 GAAATGAGCAACCTTAGAACTTTCTAGGCCCTGG-CAGATAATGAAATCAGTATATA 34087
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               79 SerAsnSerArgSerIleAsnAspPheAspThrArgTyrIleThrLysTyrLeuTyrMet 98
                                                                                   eTyrPheAspAsnHisSerSerAspPheGluLys
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Patent No. 6833446
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: McGrath, Annette
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                         US-09-640-211A-1308

Sequence 1108, Application US/09640211A

Sequence 1108, Application US/09640211A

Patent No. 6833446

GENERAL INFORMATION:
APPLICANT: Shenk, Michael A.
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A

CURRENT FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 2368

SOFTWARE: FagtSEQ for Windows Version 4.0
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Best Local Similarity:
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LENGTH: 345
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Sequence 17543 Application US/09949016

Sequence 17543 Application US/09949016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 17543

LENGTH: 36546
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                                                                                                                              SerAsnSerArgSerIleAsnAspPheAspThrArgTyrIleThrLysTyrLeuTyrMet
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Mismatches:
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US-09-949-016-17543
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, OTHER INFORMATION: n means any nucleotide US-09-270-767-10919
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US-09-270-767-10919
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Sequence 31207, Application US/09270767

Sequence 1207, Application US/09270767

Patent No. 6703491.

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENION: Nucleic acids and proteins of Drosophila melanogaster.

TITLE OF INVENION: NUMBER: US/09/270,767

CURRENT APPLICATION NUMBER: US/09/270,767

NUMBER OF SEQ ID NOS: 62517

SOFUTWARE: Patentin Ver. 2.0

LENGTH: 494
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US-09-270-767-14937/c
Sequence 14937, Application US/09270767
Petent No. 6703491
GENERAL INFORMATION:
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Best Local Similarity:
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                             TYPE: DNA
ORGANISM: Pinus
                                                            US-09-640-211A-1824
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Patent No. 6703491

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REPRENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10919
LENGTH: 2274
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 14937
LENGTH: 539
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TYPE: DNA
CRGANISM: Eucalyptus grandis
US-09-640-211A-255
           LENGTH: 541
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                                                              139 ACCAAGTCCAGGGAGAGC-----TGGACCGAGGAGGAGCACGACAAGTTCCTCGAG 189
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           51
ProAspargTrpHisAsnValAlaLysAlaValGlyGlyLysThrValGluGluValLys
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Sequence 255, Application US/09640211A
Sequence 255, Application US/09640211A
Selected No. 693446
GENERAL INFORMATION:
APPLICANT: Wood, Marthew
APPLICANT: McGrath, Annette
APPLICANT: Glann, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REPRENCE: 11000.1021C1/U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT PILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                              Decould 144

Sequence 2026, Application US/09640211A

Sequence 2026, Application US/09640211A

Patent No. 683446

GENERAL INFORMATION:

APPLICANT: Worderly, Annette

APPLICANT: McGrath, Annette

APPLICANT: GENERAL MACHAW

TITLE OF INVENTION: Compositions and Methods for the

TITLE OF INVENTION: Modification of Gene Transcription

FILE REFERENCE: 11000.10211U

CURRENT APPLICATION NUMBER: US/09/640,211A

CURRENT FILING DATE: 2000-08-16

NOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2026

LENGTH: 450
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US-09-640-211A-2026
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                                                                                                                                                                                                                                                            GlyGlyLygThrValGluGluValLysArgHis-----TyrAspIleLeuValGlu 59
                                                                                                                                                                                                      23 AlaLeuAlaValTyrAspLysAspThrProAspArgTrpHisAsnValAlaLysAlaVal
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124
128
128
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Conservative:
Mismatches:
Indels:
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31.6%
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Best Local Similarity:
Query Match:
Alignment Scores:
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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Total number

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Mdlv3 403
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Mararyota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
                                                                       Mdas9007G
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BNAF0581E Mustard flower buds Brassica rapa cDNA, mRNA sequence.
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Lim,C.O., Kim,H.Y., Kim,M.G., Lee,S.I., Chung,W.S., Park,S.H.
Hwang,I. and Cho,M.J.
Expressed sequence tags of Chinese cabbage flower bud cDNA
Plant Physiol. 111 (2), 577-588 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Lim,C.O., Kim,M.G., Hwang,I. and Cho,M.J. Plant Molecular Biology and Blotechnology Research Center Email: pmbbrc@nongae.gsnu.ac.kr. Location/Qualifiers
                                          AJT68574
CO0994824
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CO281695
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/db_xref="texon:3711"
/clone_lib="Whistard flower buds"
/note="Devel_stage = flower bud
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    .446
    /organism="Brassica rapa"

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BU890694 P040E03 P
CB920052 VVD058F11
CB919185 VVD042D03
BU66323 MC01026A1
BU822353 UB36DPB08
CV232994 WS0199.B2
                                                                                                                                                 March 10, 2006, 19:19:36 ; Search time 3742 Seconds (without alignments) 1575.407 Million cell updates/sec
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                                                                                                                                                                                                                                                                                              126
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                                                                                                                                                                                                                                                                                              ......HSSDFEKFSQKVLVSYISLV
                   GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                        - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41078325 seqs, 23393541228 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of hits satisfying chosen parameters:
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Database

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.

E 1 (bases 1 to 626)
S Cushman, J.C.
An expressed sequence tag database for abiotic stressed berries of Vitis vinifera var. Chardonnay
L Contact: Cushman JC
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
                                                                                                                                                                                                                                                                                                                                          VVD058F11 350737 An expressed sequence tag database for abiotic stressed berries of Vitis vinifera var. Chardonnay Vitis vinifera CDNA clone VVD058F11 5, mRNA sequence.
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ECORI; Site_2: XhoI"
                          SerAsnSerArgSerSerIleSerProTrpThrPheSerGlnAsnLysMetPheGluArg 22
                                                                                                                                                                                                   63 AsnijegjuThrGjyArgValProLeuProAsnTyrLysThrPheGluSerAsnSerArg 82
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PCR PRimers
PCRWARD: T3 20mer
BACKWARD: T7 21mer (backward)
Plate: 058 row: F column: 11
Seg primer: T3 20mer
High quality sequence stop: 626.
High quality sequence stop: 626.
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/db_xref="taxon:29760"
/clone="VVD058F11"
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Vitis vinifera
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The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries

Unpublished (2002)

Contact: BHALERAO RUPALI R.

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Fax: +46 90 786 6576

Email: rupali.bhalerao@plantphys.umu.se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
                                                                                                                                                                         76 ATGCCTCAAGTTCTATGAGC-----TCCTCTTGGACGTCTAAGCAAATAAGATATTC 129
                                                                                                                                                                                                                                      40
                                                                                                                                                                                                                                                                                     41 AlaValGlyGlyLysThrValGluGluValLysArgHisTyrAspIleLeuValGluAsp 60
                                                                                                                                                                                                                                                                                                                                                  61 LeulleAsnileGluThrGlyArgValProLeuProAsnTyrLysThrPheGlu---- 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="petioles"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Lamiales; Pedaliaceae; Sesamum.
                                                                                                                                       208 AAAGCCTTTGAAGAGGCGCTTGCAGTGTATGACAAGGACACCCCTGACCGCTGGTACAAT 267
                                                                                                                                                                                                                                                                                                                                           LysMetPheGluArgAlaLeuAlaValTyrAspLysAspThrProAspArgTrpHisAsn 37
                                                                                                                                                                                                                                                                                                                      58 ValGluAspLeulleAsnIleGluThrGlyArgValProLeuProAsnTyrLysThrPhe 77
                                                                                                                      MetAlaSer-----AsnSerArgSerSerIleSerProTrpThrPheSerGlnAsn 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Comparative analysis of Expressed Sequence Tags between Sesamum indicum and Arabidopsis thaliana developing seeds Unpublished (2003)
Contact: Suh, Mi Chung
Graduate School of Biotechnology, Korea University
II, 5-78, Anam-dong, Sungbuk-ku, Seoul 136-701, Rep. of Korea Fax: 82 2 927 9028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Sesamum indicum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BU668323 474 bp mRNA linear
MC01026A10 MC01 Sesamum indicum cDNA, mRNA sequence.
BU668323
                                                                                                                                                                                                                                                                                                                                                                                                             388 GGAGCTAGTGGCCGGTCCAACATGAGCGACCAGGAAAAGAGG 429
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sesamum indicum (sesame)
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Corganism="Vitis vinifera"

/mol_type="mRNA"

/db_xrefp="reacon:29760"

/clone="VVD042D03"

/tissue_type="berries"

/dev_stage="mixed; 8, 9, 11, 13, 15, 16 weeks daf"

/clone_lib="An expressed sequence tag database for abiotic

stressed berries of Vitis vinifera var. Chardonnay".

/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:

ECORI; Site_2: XhoI"
                                                                                                                                                       Vitis vinifera
Vitis vinifera
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons,
rosida, Vitaceae, Vitis.
1 bases I to 662)
Cushman, J.C.
                                                                                                                                                                                                                                                                                  LysMetPheGluArgAlaLeuAlaValTyrAspLysAspThrProAspArgTrpHisAsn 37
                                                                                                                                                                                             38 ValAlaLysAlaValGlyGlyLysThrValGluGluValLysArgHisTyrAspIleLeu 57
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                                                                MetAlaSer-----AsnSerArgSerSerIleSerProTrpThrPheSerGlnAsn 17
                                                                                                                                                                                                                                                             58 ValGluAspLeulleAsnileGluThrGlyArgValProLeuProAsnTyrLysThrPhe 77
                                                                                                                                                                                                                                                                                                                                                      388 GGAGCTAGTGGCCGGTCCAACATGAGCGACCAGGAAAAGAGG 429
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 Gaps:
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Vitis vinifera var. Chardonnay
Unpublished (2002)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
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Tel: 775-784-1918
Fax: 775-784-1650
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Populus trichocarpa (Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Beamatophyta; Malpighiales; Salicaceas; Saliceae; Populus. Trosids; eurosids; Malpighiales; Salicaceas; Saliceae; Populus. (Dases 1 to 624)

Ralph, S., Cooper, D., Kolosova, N., Oddy, C., Butterfield, Y., Kirkpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G., Babakaiff, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A., Mayo, M., Moran, J., Olson, T., Wong, D., Ritland, C.E., Siddiqui, A., Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritland, K. and Bohlmann, J.
                                                                                                                                                                                                                   624 bp mRNA linear EST 21-SEP-2004 WS0199 E21 E24 PT-DX-N-A-10 Populus trichocarpa cDNA clone WS0199 E24 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The poplar transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries
Unpublished (2004)
                       219 GGTGGCAAGTCTCCTGAAGAAGTTAAGAGGCACTATGATCGTCTCGTGGAAGATCTCGTG 278
                                                                                        43 GlyGlyLysThrValGluGluValLysArgHisTyrAspIleLeuValGluAspLeuIle 62
                                                                   63 ABNILGGluThrGlyArgValProLeuProAenTyrLysThrPheGluSerAenSerArg 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Joerg Bohlmann
Genome BC forest genomics program
Genome BC forest genomics brolumbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 123
Tel: 1-604-822-0282
Pax: 1-604-822-2114
                                                                                                                                                                                                                                                                                                                                                Populus trichocarpa (Populus balsamifera subsp. trichocarpa)

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    /organism="Populus trichocarpa"

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Plate: WSQ199 row: E column: 'High quality sequence stop: 624
POLYA=Yes.
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1986DPB08 Populus tremula cambium cDNA library Populus tremula CDNA
5 prime, mRNA sequence.
BU822353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaLeuAlaValTyrAspLysAspThrProAspArgTrpHisAsnValAlaLysAlaVal 42
                                                                                      17 AsniyaMetPheGluArgAlaLeuAlaValTyrAspLysAspThrProAspArgTrpHis 36
                                                                                                                                                           37 AsnValAlaLysAlaValGlyGlyLysThrValGluGluValLysArgHisTyrAspile 56
                                                                                                                                                                                                                                LeuValGluAspLeulleAsnIleGluThrGlyArgValProLeuProAsnTyrLysThr 76
                       1 MetAlaSerAsnSer-----ArgSerSerIleSerProTrpThrPheSerGln 16
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                                           /tiğsue_type="cambium"
/clone_lib="Populus tremula cambium cDNA library"
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Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalerao@plantphys.umu.se.
Location/Qualifiers
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/db xref="taxon:113636"
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/clome_lib="PT-DX-N-A-10"
/clome_lib="PT-DX-N-A-10"
/clome_lib="PT-DX-N-A-10"
/clome_lib="PT-DX-N-A-10"
/clome_lib="PT-DX-N-A-10"
/note="Vector: pBluescript II SK (+) XR; Site 1: EcoRI (5')
end of cDNA); Site_2: MhoI (3') end of cDNA); Outer xylem
from 5 year cold trees harvested every two weeks between
April and October of 2002 at the University of British
Columbia south campus farm in Vancouver, British Columbia.
mRNA was isolated from each tissue source independently
and equal quantities of mRNA from each tissue were then
pooled. cDNA was prepared from 5 micrograms of mRNA and
directionally ligated into the pBluescript II SK (+) XR
vector using the pBluescript II XR cDNA Library
Construction Kit according to manufacturer's instructions
with modifications (Stratagene). Plasmid DNA was then
transformed by electroporation into DHIOB cells
(Invitrogen) for propagation. Normalization was applied
according to published methods [Bonaldo M.F. et al. (1996)
Genome Research 6(9):791] in order to reduce the abundance
of highly expressed transcripte."
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Bukaryota; Viridiplantae; Streptophyta; Core eudicotyledons;
Fosmatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 256)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          390 TACATAGAATCCGGCCAAAGCCCCTCTGCCGAATTACAAGCCCTCTGGCAGCAATGGTAGA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 SerAsnSerArgSerSerIleSerProTrpThrPheSerGlnAsnLysMetPheGluArg
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Populus trichocarpa
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Maroliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I, Malpighiales; Salicaceae; Salicace; Populus. I (bases 1 to 627)
Ralph,S., Cooper,D., Kolosova,N., Oddy,C., Butterfield,Y., Kirkpatrick,R., Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G., Babakaiff,R., Brown-John,M., Chand,S., Featherstone,R., Masson,A., Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddiqui,A., Bohlmann,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The poplar transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries
multiple cDNA libraries
Combabilabed (2004)
Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 123
Tel: 1-604-822-0282
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/organism="Populus trichocarpa"
/mol type="mRNA"
/cultivar="VT-125"
/db xref="teaxon:3694"
/clone="WS01916_F23"
                                                                                                                                                                         Gaps:
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Plate: WS01916 row: F column:
High quality sequence stop: 627
PoLYAPYES.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus
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                                                                                                                       1.598 | organism="Populus euphratica" | mol_type="mRNA" | mol_type="mRNA" | mol_type="mRNA" | mol_type="leaxon:75702" | clone="Po000100019D06F1" | tissue_type="leaf" | dev_stage="adult" | clone="country: Israel:Ein Avdat" | note="country: Israel:Ein Avdat"
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Apple Functional Genomics grant - NSF 0321702
Washington University School of Medicine
Department of Biosciences, Plant Physiology
University of Helsinki
FIN-00014 Helsinki, Finland.
Location/Qualifiers
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                       Contract: Joseph K. Eckel
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Email: eckeremealk.edu
This is single pass sequence recovered from the left border of
This is single pass sequence recovered from the left border of
This is single pass sequence recovered from the left border of
AL197520.

Class: TDNA tagged.
Location/Qualifiers
1. 256
/ Cranism="Arabidopsis thaliana"
/ Mol type="genomic DNA"
/ Glone="Portype="Col-0"
/ db xrefe="taxon:3702"
/ clone="Portype="Col-0"
/ db xrefe="Textabledopsis thaliana TDNA insertion
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence
directly sequenced to determine the genomic sequence
directly sequenced to determine the genomic sequence
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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Populus euphratica
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Varidiplantae, Streptophyta; Core eudicotyledons;
rosids; eurosids 1; Malpighiales; Salicaceae; Saliceae; Populus.
1 (basea 1 to 590 E.R., Vinocur, B., Altman, A., Teichmann, T., Ottow, E.A., Polle, A., Dillianov, D., Afif, D., Triboulot, M.B., Gene expression in desert leaves
Unpublished (2004)
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         Joseph R. Ecker
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/lab host="DH10B ampicillin resistant"
/clone_lib="Apple_EST_Mdas"
/clone_lib="Apple_EST_Mdas"
/note="Vector: pBluescript II SK (+); Site_I: XhOI;
Site_2: EcoRI; Total RNA was extracted from freeze dried
leaf tissue, using the method described by Wang and Vodkin
(Plant Molecular Biology Reporter 12:132-145, 1994).
POlyAh + mRNA was isolated from total RNA using the
PolyATtract mRNA leolation system III (Promega). The
Ibbary was prepared using the Stratagene pBluescript II
XR CDNA library construction kit. Complementary DNA was
synthesized from mRNA using a Poly (dT) sequence with a
XROI restriction site. EcoRI adapters were ligated to the
blunt ended cDNA fragments followed by restriction with
XhoI. The CDNA insert is protected from XhoI digestion via
methylation during first strand cDNA synthesis. The cDNA
fragments were directionally cloned into the EcoRI-XhoI
restriction site of the pBluescript vector. The ligated
CDNA fragments were transformed into E. coli ElectroMax
DH10B host cells. Transformation efficiency: 1.0E+04
Average insert Size by PCR: 1290 bp"
4444 Forest rain.

Tel: 314 286 1800
Fax: 314 286 1810
Email: estGwatson.wustl.edu
Library material provided by S. Korban/H. Aldwinckle/ M. Malnoy
Library material provided by S. Korban/H. Aldwinckle/ M. Malnoy
Library constructed by D.O.Gonzalez/L.Vodkin Library sequenced by
Washington University Genome Sequencing Center
This trace has been recalled with phred
original value before phred recall for SL was 118
original value before phred recall for SR was 873.

Location/Qualifiers

Anmestica"
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/tissue type="Leaves challenged with apple scab (Venturia
inaequalis)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 ValGluAspLeulleAsnIleGluThrGlyArgValProLeuProAsnTyrLysThrPhe 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 GTGGCCAAAGCGGTCGGCGCAAAACACCGGAGGAAGTCAAGAGCACTATGAGGTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MetMetLeuSerIleTyrPheAspAsnHisSerSerAspPheGluLys 113
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62
12
17
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                               /organism="Malus x domestica"
/mol_type="mRNA"
/cultivar="GoldRush"
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Matches:
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63.8%
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Pred. No.:
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// Organism="Windle x domestica"
// organism="Windle x domestica"
// db xref="caodRush"
// culfivar="GoldRush"
// culfivar="GoldRush"
// inche="Windle xexn:3750"
// inche="Windle xexn:3750"
// inche="Windle xexn:3750"
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// inche="Veccr: Bluescript II SK (+); Site 1: NotI;
// inche="Veccr: Bluescript II SK (+); Site 1: NotI;
// inche="Veccr: Bluescript II SK (+); Site 1: NotI;
// inche="Veccr: Bluescript II SK (+); Site 1: NotI;
// inche="Veccr: Bluescript II SK (+); Site 1: NotI;
// inche="Veccr: Bluescript II SK (+); Site 1: NotI;
// inche="Veccr: Bluescript II SK (+); Site 1: NotI;
// inche="Veccr: Bluescript II SK (+); Site 1: NotI;
// inche x bluescript II SK (+); Site 1: NotI;
// inche x bluescript II SK (+); Site 1: NotI;
// inche x bluescript II Stage 4 (afterpollination)
// inche x bluescript II Stage 2 (balloon)
// inche x bluescript II Tag identification when sequencing from 3 end: Stage 1 (bud) insert
// inche x bluescript II Tag identification when sequencing from 3 end: Stage 1 (bud) insert
// insert 18 (A)TCGGA; Stage 2 (balloon)
// insert 18 (A)TCGGA; Stage 3 (open)
// insert bluescript II Tage x both ends and then digested with
// insert Stage 3 (open)
// insert bluescript II SK (+) phagemid
// insert bluescript II SK (+) phagemid
// vector (Strat EcoRI adaptor) GATATCGATTGGG (End
// ECORI adapter Tag) TGCGA (End
// ECORI adapter) (Start Insert)
// insert Tag) TGCGA (End
// insert Tag) Tago (End
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Bukaryora;
Bukarora;
Bukarora;
Bukarora;
Bukarora;
Bukaroka;
Bukara;
B
                                               EST 14-JUN-2004
COUSZ301

MGFW2057018.yl Mdfw Malus x domestica cDNA clone Mdfw2057018 5'
similar to TR:Q9SIJ5 Q9SIJ5 ATZG21650 PROTEIN. ;, mRNA sequence.
CO052301
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Library materials provided by: Schuyler S. Korban Library
Library materials provided by: Schuyler S. Korban Library
constructed by: A. Hernandez / K. Gasic Library sequenced by:
Washington University Genome Sequencing Center
Washington University Genome Sequencing Center
Seq primer: -40UP from Gibco
High quality sequence stop: 456.
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/organism="Malus x domestica"
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beforeamplification was 1.1x10°6 cfu (colony forming units). The background of empty clones was less than 1%. Inserts ranged from 0.5kb to 3 kb, as determined by PCR. Purified plasmid DNA from the primary library was converted to single-strandedcircles and used as a template for PCR amplification using the T7 and T3 priming sites flanking the cloned cDNA inserts. The purified PCR products, representing the entire cloned cDNA population, were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 hours at 30C. Unhybridized bNA rendered partially double-stranded and electroporated into DNIOB cells to generate the normalized library. The total number of clones with insert was 9x10°6 cfu. Background of empty clones was less than 1%."
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1 (bases 1 to 463)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of CDNA in Arabidopsis thaliana: Generation of I2,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     463 bp mRNA linear EST 18-FEB-2004 AV440717 Arabidopsis thaliana above-ground organ two to six-week old Arabidopsis thaliana cDNA clone APZ07C09_f 3', mRNA sequence. AV440717
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Kazusa DNA Research Institute
Yana 153-3. Kisarazu, Chiba 292-0812, Japan
Email: asamizuskazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 TCTTCCTCGAGGAATTTCAACTCCTCGTGGACGCCGAAGGAGAAACAAGCTGTTCGAGAAG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 GCGCTGGCCGTGTACGACAAGGACACGCAGGACCGCTGGCATAATGTGGCCCAAGGCCGTC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42
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Conservative:
Mismatches:
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Arabidopsis thaliana
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EST.
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292.00
87.8%
71.6%
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Best Local Similarity:
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DEFINITION
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ORGANISM
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AV440717/c
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TITLE
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PUBMED
COMMENT
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/organism="Arabidopsis thaliana" /mol\_type="mRNA"

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Populus trichocarpa x Populus deltoides
Populus trichocarpa x Populus deltoides
Populus trichocarpa x Populus deltoides
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Magnollophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
I (Bases I to 787). Kolosova,N., Oddy,C., Butterfield,Y.,
Kirkpatrick,R., Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G.,
Babakaiff,R., Brown-John,M., Chand,S., Featherstone,R., Masson,A.,
Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddiqui,A.,
Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., Ritland,K. and
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Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 GCCGTTGGCGGCAAATCAGCTGAAGAAGTAAGGCGACACTACGAGCTCCTCATTAGGGT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nSerArgSerile-AsnAspPheAspThrArgTyrIleThrLysTyrLeuTyrMetMetL 100
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                                                  /dev_stage="two to six-week old"
/dev_stage="two to six-week old"
/clone_lib="Arabidopsis thaliana above-ground organ two t
six-week old"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
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Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeulleAsnIleGluThrGlyArgValProLeuProAsnTyrLysThr-PheGluSerAs
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/clone="AP207c09_f"
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                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
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CV281695.1 GI:52534670
                                                                                                                                                                                                                                          1.45e-28
290.50
70.4%
51.3%
                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                              Alignment Scores:
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AUTHORS
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/Jab hose-we. Could DH10B cells"
/clone lib="WS-PP-N-A-12"
/clone lib=
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1 (Bases I to 906).

Ralph, S., Kolosova, N., Oddy, C., Cooper, D., Butterfield, Y., Kirkpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G., Babakiiff, R., Brown-John, M., Chand, S., Faetherstone, R., Masson, A., Siddiqui, A., Holt, R., Yong, D., Friedmann, M.F., Ritland, C.E., Siddiqui, A., Holt, R., Yong, D., Friedmann, M.F., Ritland, C.E., Ritland, K. and Bohlmann, J.

The spruce transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 123
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/dev stage="mature trees harvested at Vernon, British
Columbia in 2001"
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Matches:
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Email: bohlmann@msl.ubc.ca
Plate: WS02616 row: G column: 18
High quality sequence stop: 906.
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                                                                                                                                Picea glauca (white spruce)
                                                 GI:70623505
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No
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AUTHORS
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            ACCESSION
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab hose = "B. coli DH10B T1 phage resistant cells"
/clone_lib="PTXD-IL-N-A-9"
/clone_lib="VetCor: pBluescript II SK (+) XR; Site 1: EccRI (5'
end of cDNA); Site 2: Xhol (3' end of cDNA); Sapling trees
two metres in height and grown under greenhouse conditions
were exposed to continuous feeding by Malacosoma disstria
Hubner (forest tent caterpillar) mid-instar larvae caged
on the sapling using mesh bags. Mature leaves from within
the caged region were collected 2 hours, 12 hours, 24
hours and 48 hours after the onset of treatment. mRNA was
isolated from each tissue source independently and equal
quantities of mRNA from each tissue were then pooled. cDNA
was prepared from 5 micrograms of mRNA and intectionally
ligated into the pBluescript II SK (+) XR vector using the
pBluescript II XR cDNA Library Construction Kit according
to mannifacturer's instructions with modifications
(Stratagene). Plasmid DNA was then transformed by
electroporation into DH10B cells (Invitrogen) for
propagation. Normalization was applied according to
published methods [Bonaldo M.F. et al. (1996) Genome
Research 6(3):791] in order to reduce the abundance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DR559298 906 bp mRNA linear EST 08-JUL-2005 WS02616.B21_G18 WS-N-A-12 Picea glauca cDNA clone WS02616_G18 3, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                      /organism="Populus trichocarpa x Populus deltoides"
/mol_type="mRNA"
/cultivar="H11-11"
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Tel: 1-604-822-0282
Fax: 1-604-822-2114
Email: bohlmann@msl.ubc.ca
Plate: WS0182 row: J column: 21
High quality sequence stop: 787
POLYA=Yes.
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/clone="WS0182_J21"
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        617 TTAGCCATTATGACAAAGACCTCTGACTAATGGGCTTCTGGTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTTGGTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTGGTTGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTGGTTGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTG
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Database :

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Minimum DB Maximum DB

Perfect score:

Sequence:

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Scoring table:

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656 473 343 327.5

Score

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New transgenic plants for producing commercially or agriculturally useful plants having improved tolerance to drought, shade and low nitrogen
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                               transcription factor; transgenic plant; agriculture; drought resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluArgAlaLeuAlaValTYrAspLy8AspThrProAspArgTrpHi8AsnValAlaLy8
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tolerant plant-related transcription factor gene SeqID975
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05-DEC-2003; 2003US-0527658P.
05-FEB-2004; 2004US-0542928P.
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Repetti P, Kumimoto RW,
Sherman BK, Morrison TA,
Zhang JZ, Hempel FD, Lik
                                                    stress tolerance; gene;
                                                                                 Arabidopsis thaliana
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Best Local Similarity:
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                                                                                                                                                                                                                                                                 The invention relates to a transgenic plant that possesses a plant transformation vector comprising a nucleotide sequence that encodes a peronospora parasitica resistant (PPR2) protein, or a PPR2 orthologue. The transgenic plant is useful in generating plants with a pathogen resistance phenotype. The PPR2 nucleic acids and proteins of the hivornion are useful in the generation of genetically modified plants having a modified pathogen resistance phenotype. The present DNA sequence encodes an Arabidopsis thaliana PPR2 protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerileTyrPheAspAsnHisSerSerAspPheGluLysPheSerGlnLysValLeuVal 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGATATATTTTGATAATCATTCTAGTGATTTTGAGAAATTCTCTCAAAAAGTTCTTGTA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 CTCATCAACATCGAGACTGGTCGTGTCCCTTGCCCAATTACAAGACCTTCGAATCTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluArgAlaLeuAlaValTyrAspLysAspThrProAspArgTrpHisAsnValAlaLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MetAlaSerAsnSerArgSerSerIleSerProTrpThrPheSerGlnAsnLysMetPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGGCGTCAAACTCAAGAAGTTCAATCTCACCATGGACGTTTAGTCAAAACAAGATGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaValGlyGlyLysThrValGluGluValLysArgHisTyrAspIleLeuValGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuileAsnileGluThrGlyArgValProLeuProAsnTyrLysThrPheGluSerAsn
                                                                                                                                                                  New transgenic plants with increased resistance to pathogens due to altered expression of Peronospora Parasitica Resistant gene (PPR2), useful for generating plants with a pathogen resistance phenotype.
                                                              ່ວ
                                                                   Westerlund
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 381 BP; 122 A; 76 C; 76 G; 107 T; 0 U; 0 Other;
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126
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Matches:
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                                                                  Bates SR,
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                                                                  Liu
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 24-APR-2002; 2002US-0375333P.
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656.00
100.0%
100.0%
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                                                                   Lammers A,
                                                                                                                   WPI; 2003-865582/80.
P-PSDB; ADF43566.
                                  (AGRI-) AGRINOMICS
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Best Local Similarity:
                                                                Federspiel N,
Fitch JR;
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75.0%
52.3%
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Best Local Similarity:
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                                                                                                                                          Alignment Scores:
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09-MAR-1999;
23-MAR-1999;
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29-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proceins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The sequences can be used to produce transgenic plants which overexpress (II) where the transgenic plant has an altered trait as compared to a non-transgenic plant has an altered trait as compared to an altered trait selected from increased tolerance to cold, increased tolerance to increased tolerance to low introgen conditions, increased tolerance to cold, increased tolerance to old increased tolerance to low phosphate conditions, increased tolerance to low phosphate conditions, increased tolerance to cold increased tolerance to make the process of the process
                                                                                                                                                                   Plant; transcription factor; transgenic plant; abiotic stress tolerance; sometic stress tolerance; cold tolerance; heat tolerance; low nitrogen tolerance; low hosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reuber TL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to novel plant transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adam LJ, R
Sherman BK;
                                                                                                                                   Transcription factor G2723 coding sequence, SEQ ID 509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Creelman RA,
, Keddie JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 509; 510pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratcliffe O, C1
V, Dubell AN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                (MEND-) MENDEL BIOTECHNOLOGY INC.
                                      ADO62042 standard; DNA; 279 BP.
                                                                                                                                                                                                                                                                                                                                                                               18-SEP-2002; 2002US-0411837P.
17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
                                                                                                                                                                                                                                                                                                                                                18-SEP-2003; 2003WO-US030292.
                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jiang C, Heard JE,
Riechmann JL, Haake
                                                                                                                                                                                                                                                  Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2004-330163/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-330163/
P-PSDB; ADO62043
                                                                                                                                                                                                                                                                                  WO2004031349-A2.
                                                                                                      15-JUL-2004
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                                                                      ADO62042;
      RESULT 3
ADO62042
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content, altered seed protein content, altered seedprenyl content, altered leaf prenyl lipid content, increased anthocyanin levels, and decreased anthocyanin levels. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GAGAGGCTTTAGCCGTTTACGATAAAGACACTCCCGACCGTTGGCAAAACGTGGCTAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ArGGCCTCTAGATCTAGAGCTCGAGCTCTTGGACGTCTAAGCAAAACAAGATGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 GluArgAlaLeuAlaValTyrAspLysAspThrProAspArgTrpHisAsnValAlaLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 AlaValGlyGlyLysThrValGluGluValLysArgHisTyrAspIleLeuValGluAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      MetAlaSerAsnSerArgSerSerIleSerProTrpThrPheSerGlnAsnLysMetPhe
                                                                                                                                                                  Sequence 279 BP; 86 A; 56 C; 65 G; 72 T; 0 U; 0 Other;
                                                                                                                                                                                                                                          279
69
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16
1
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                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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99US-0129845P.
99US-0130077P.
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99US-0123548P.
99US-0125788P.
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99US-0126785P.
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9US-0130510 9US-0130510 9US-0131449 9US-0132404 9US-0132486 9US-0132486 9US-0132486 9US-0132486 9US-0132486 9US-0132486 9US-0132486 9US-0132863	99US-0134768P. 99US-013124P. 99US-013124P. 99US-0131553P. 99US-0135629P. 99US-0135021P. 99US-0135021P. 99US-0137222P. 99US-0137222P. 99US-0137222P. 99US-0137222P. 99US-0137452P. 99US-0139454P. 99US-0139453P. 99US-0139453P. 99US-0139453P. 99US-0139454P. 99US-0139454P. 99US-0139454P. 99US-0139454P. 99US-0139454P.	905 - 0140359 905 - 0140354 905 - 0140859 905 - 0140859 905 - 0141287 905 - 0141287 905 - 014235 905 - 014236 905 - 014236 905 - 0144086 905 - 0144086
3. APR. 1999 8. APR. 1999 8. APR. 1999 0. APR. 1999 4. O. APR. 1999 5. MAY. 1999 6. MAY. 1999 4. MAY. 1999 4. MAY. 1999	18-MAY-1999; 20-MAY-1999; 21-MAY-1999; 24-MAY-1999; 25-MAY-1999; 27-MAY-1999; 28-MAY-1999; 28-MAY-1999; 38-JUN-1999; 38-JU	3UUN-1999 4UUN-1999 8UUN-1999 9UUN-1999 9UUN-1999 9UUN-1999 9UUN-1999 9UUN-1999 9UUN-1999 9UUN-1999 9UUN-1999 9UUN-1999 9UUN-1999 9UUN-1999 9UUN-1999 9UUN-1999 9UUN-1999 9UUN-1999 9UUN-1999 9UUN-1999 9UUN-1999 9UUN-1999
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0US-0144632P 9US-01448848 9US-0144814P 9US-0145086P 9US-0145086P 9US-0145089P 9US-0145089P 9US-014513P 9US-014513P 9US-0145213P 9US-0145213P 9US-0145213P 9US-01452313P 9US-0145313P 9US-0145313P 9US-0145318P 9US-0145318P	905 01467899 905 01470389 905 01472049 905 01472049 905 01472059 905 01474169 905 01474169 905 01474169 905 01474169 905 01481419 905 01481718 905 01481718 905 01481718 905 014818419 905 0149188419 905 0149188419 905 0149189 905 0149189 905 0149189 905 0149929 905 0149929 905 0149929 905 0149929 905 0149929 905 0149929 905 0149929 905 0149929 905 0149929 905 0149909 905 01499929 905 0149909	99US-0151066P. 99US-0151080P. 99US-0151303P. 99US-0151330P. 99US-0151330P. 99US-0153788P. 99US-0153788P. 99US-0153788P. 99US-0153788P. 99US-015408P. 99US-015408P. 99US-0155488P. 99US-0155488P. 99US-0155488P. 99US-0155488P. 99US-0155488P. 99US-0155488P. 99US-015569P. 99US-015569P. 99US-015569P. 99US-015569P. 99US-015929P. 99US-015929P. 99US-015929P. 99US-015929P. 99US-015929P.
0.70L-1999 1-70L-1999 1-70L-1999 1-70L-1999 2-70L-1999 2-70L-1999 3-70L-1999 3-70L-1999 3-70L-1999 3-70L-1999 3-70L-1999 3-70L-1999 3-70L-1999 3-70L-1999 3-70L-1999	2MG-1999 3AUG-1999 4AUG-1999 5AUG-1999 6AUG-1999 9AUG-1999 9AUG-1999 0AUG-1999 0AUG-1999 0AUG-1999 0AUG-1999 0AUG-1999 0AUG-1999 0AUG-1999 0AUG-1999 0AUG-1999	ANG-19999 ANG-19999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cotton; 88; plant, cold tolerance; growth rate; cell cycle pathway; drought tolerance; plant disease resistance; galactomannan; lignin; plant growth regulator; heat tolerance; herbicide tolerance; homologous recombination; extreme osmotic condition tolerance; pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
                                                                                                                                                                                                                                                                                                                                                                                       30 AspThrProAspArgTrpHisAsnValAlaLysAlavalGlyGlyUysThrValGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                 5 TCTTCTTGGACGTCTAAGCAAACAAGATGTTCGAGAGGCCTTTAGCCGTTTACGATAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerProTrpThrPheSerGlnAsnLysMetPheGluArgAlaLeuAlaValTyrAspLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProLeuProAsnTyrLysThrPheGlu-----SerAsnSerArgSerIleAsnAspPhe
                                                                                                                                                                                                                                                                                                                                                                                                                             50 VallysArgHisTyrAsplleLeuValGluAspLeurleAsnIleGluThrGlyArgVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspThrArgTyrileThrLysTyr------LeuTyrMetMet
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67
119
2
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Conservative:
Mismatches:
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990S-0159637P.
990S-0159638P.
990S-015964P.
990S-0160741P.
990S-016076P.
990S-0160714P.
990S-016091AP.
990S-0160981P.
990S-0160981P.
990S-0160981P.
                                                                                                                                  99US-0161405P.
99US-0161406P.
99US-0161359P.
99US-0161361P.
99US-0161361P.
99US-0161920P.
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99US-0162142P
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327.50
73.2%
69.1%
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Best Local Similarity:
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                             21-001-1999;
21-007-1999;
21-007-1999;
21-007-1999;
22-007-1999;
22-007-1999;
22-007-1999;
25-007-1999;
25-007-1999;
26-007-1999;
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26-OCT-1999;
28-OCT-1999;
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The invention relates to a recombinant polymucleotide comprising any of the 58798 Cotton plant cDNA sequences mentioned in the specification.

Also a recombinant polypeptide comprising any of the 58798 amino acid sequences mentioned in the specification and producing a plant having an improved property.

Comprises transforming a plant with a recombinant construct comprising a promoter region functional in a plant cell operably joined to a promoter region functional in a plant cell operably joined to a promoter region functional in a plant cell operably joined to a polymucleotide comprising a coding sequence for a polypeptide associated with the property, and growing the transformed plant. The polypeptide is useful for improving plant cold tolerance for a manipulating growth rate in plant cells by modification of the cell cycle pathway, improving plant coll tolerance to plant disease, contoucing galactomannan (or lignin or plant growth regulators) improving plant heat tolerance, improving plant tolerance to herbicides, increasing colling in plants, improving plant tolerance conditions or plant growth and development under a least one stress condition; The addor content, improving yield by modification of photosynthesis, wolfying seed oil or protein yield by modification of photosynthesis, or improving yield by providing improved plant growth and development under at least one stress condition. The constructs, in physical arrays of molecules, as plant breeding markers, or in computer-based storage and analysis systems. The present sequence constructs and a plant collection but the sequence constructs and a plant collection but collection be invention where the sequence constructs are constructed and polypeptide may also be used in recombinant DNA constructs. The sequence constructs are constructed and polypeptide and polypeptide may also be used in recombinant plant cDNA of the invention worth the sequence constructs and constructs are necessarily and an analysis systems. The sequence constructs are constructed a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence. Organization of sequence. html/DocID=20040181830. However only 6585 polymucleotide sequences were available, the remaining 52213 polymucleotides and all 58798 protein sequences were not present.
                                                                                                                                                                                                                                                                                                                                                                                    New recombinant nucleic acid molecules and polypeptides from Gossypium hirsutum, useful for producing plants with improved biological characteristics (e.g. improved plant cold or drought tolerance).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetalaSerAsnSerArgSerSerIleSerProTrpThrPheSerGlnAsnLysMetPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 270; 14pp; English.
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                                                                   29-JAN-2004; 2004US-00767795.
                                                                                                                   07-MAY-2001; 2001US-00849529.
12-DEC-2001; 2001US-00021323.
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70.0%
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                                                                                                                                                                                          (KOVA/) KOVALIC D K.
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167 GAAAGGGCTTTAGCTGTTTACGACAAGGACACCACAGATCGTTGGTACAATGTTGCTAAA 226

GluArgAlaLeuAlaValTyrAspLysAspThrProAspArgTrpHisAsnValAlaLys

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1 1917

US2004181830-A1

41 AlaValGlyGlyLysThrValGluGluValLysArgHisTyrAspIleLeuValGluAsp 60

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990S-0139453P.
990S-0139452P.
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990S-01394557P.
990S-0139456P.
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990S-0140833P.
990S-0140833P.
990S-0140832P.
990S-0141237P.
990S-0141237P.
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990S-014508P.
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11-AUG-1999;
12-AUG-1999;
16 - 70N - 1999;

17 - 70N - 1999;

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27 - 70N - 1999;

28 - 70N - 1999;

29 - 70N - 1999;

20 - 70N - 1
  Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                 Arabidopsis thaliana DNA fragment SEQ ID NO: 9536
                                                                                                                                AAC35256 standard; DNA; 508 BP.
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9908-0123180P.
9908-012564P.
9908-012564P.
9908-012664P.
9908-012664P.
9908-0120845P.
9908-0130449P.
9908-0130449P.
9908-0130449P.
9908-0131449P.
9908-0131449P.
9908-0132484P.
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990S-0138094P.
990S-0138540P.
990S-0138847P.
990S-0139119P.
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                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
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29-MAR-1999;

06-APR-1999;

06-APR-1999;

16-APR-1999;

21-APR-1999;

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23-APR-1999;

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11-MAY-1999;

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19-MAY-1999;

19-MAY-1999;

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19-MAY-1999;

10-MAY-1999;

10-MAY-1999;

11-MAY-1999;

11-MAY-1999;
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Conservative:
Mismatches:
Indels:
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99US-0148684P
99US-0148684P
99US-01491368P-
99US-0149122P-
99US-0149723P-
99US-0149923P-
99US-0149902P-
99US-0149902P-
99US-0150566P-
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990S-0159634P
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9905-0161406P-
9905-0161359P-
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              13-AUG-1999;
16-AUG-1999;
17-AUG-1999;
20-AUG-1999;
20-AUG-1999;
21-AUG-1999;
23-AUG-1999;
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26-AUG-1999;
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26-SE
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27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
01-SEP-1999;
07-SEP-1999;
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New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
                                                                          40
                                                                                                                 41 AlaValGlyGlyLysThrValGluGluValLysArgHisTyrAspIleLeuValGluAsp 60
                                                                                                                                                                               LeulleAsnileGluThrGlyArgValProLeuProAsnTyrLysThrPheGluSerAsn 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp. seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in
                                                                                                                                                                                                                                                                                                                                                                                         plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; heat tolerance; extreme osmocic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; pathway; disease resistance; yield; plant growth; plant development; seed oil; protein yield; protein yield;
 MetAlaSerAsnSerArgSerSerIleSerProTrpThrPheSerGlnAsnLysMetPhe
                                                          GluArgAlaLeuAlaValTyrAspLysAspThrProAspArgTrpHisAsnValAlaLys
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                                                                                                                                                                                                                                                                       ADX32012 standard; cDNA; 704 BP
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KOVALIC D K.
SCREEN S E.
TABASKA J E.
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US-10-697-787-2 (1-126) x AAC35256 (1-508)

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08-JUL-1999;
09-JUL-1999;
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24 - JUN - 1999;
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  Increased resistance to plant disease, for producing galactomannan, lighting nor plant growth regulators, for increasing the rate of homologous recombination in plants, for inproving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polymucleotide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeulleAsnileGluThrGlyArgValProLeuProAsnTyrLysThrPheGluSerAsn 80
                                                                                                                                                                                                                                                                                                                                   1 MetAlaSerAsnSerArgSerSerIleSerProTrpThrPheSerGlnAsnLysMetPhe 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                     AlavalGlyGlyLysThrValGluGluValLysArgHisTyrAspIleLeuValGluAsp
  cells by modification of the cell cycle pathway, for conferring
                                                                                                                                                            Sequence 704 BP; 202 A; 159 C; 121 G; 222 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana DNA fragment SEQ ID NO: 36586
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Matches:
Conservative:
Mismatches:
Indels:
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99US-0123180P.
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99US-0126264P.
99US-0126785P.
99US-0126785P.
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80.2%
66.7%
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                                                                                                                                                                                                                                   Percent Similarity:
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
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                                                                                                                                    Invention.
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990S-015088P.
990S-015088P.
990S-01508P.
19-JUL-1999;
19-JUL-1999;
20-JUL-1999;
20-JUL-1999;
21-JUL-1999;
22-JUL-1999;
22-JUL-1999;
22-JUL-1999;
22-JUL-1999;
23-JUL-1999;
22-JUL-1999;
23-JUL-1999;
23-JU
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	Length: 306 Matches: 56 Conservative: 6 Mismatches: 19 Indels: 2 Gaps: 1	2 (1-126) x AAC42715 (1-306)  MetalaserAsnSerAsnSerIseSerProTrpThrPheSerGlnAsnLy8 18
99US-0159295P 99US-0159312P 99US-0159637P 99US-0159637P 99US-0159638P 99US-0159638P 99US-0160741P 99US-0160770P 99US-0160770P 99US-0160770P 99US-0160981P 99US-0160981P 99US-0161404P 99US-0161359P 99US-0161359P 99US-0161359P 99US-0161359P 99US-0161359P 99US-0161359P 99US-0161359P 99US-0161359P 99US-0161359P 99US-0161359P 99US-0161359P	6.63e-28 286.00 : 74.7\$ ity: 67.5\$ 3.6\$	2 (1-126) x AAC42715 (1-30 MetAlaSerAenSerAenSerSerIl ATGGCATCAGGCTCAATGTCTTCTTA MetPheGluargalaLeualaValTY GCTTTGAGCGTCTAGCAGTCTA AlaLysAlaValGYGIYLYSThrVa. GCTACAGCTGTTGGTGGTAAACACC GluaspLeuIleAsnIleGluThrGI.    ::
13-0CT-1999; 14-0CT-1999; 14-0CT-1999; 14-0CT-1999; 14-0CT-1999; 21-0CT-1999; 21-0CT-1999; 21-0CT-1999; 22-0CT-1999; 22-0CT-1999; 22-0CT-1999; 25-0CT-1999; 25-0CT-1999; 26-0CT-1999;	ment Scor No.: nt Simila nt Simila Match:	US-10-697-787-2 (1-126)  Oy
* # # # # # # # # # # # # # # # # # # #	Align Pred. Score Perce Best Query DB:	SXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

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414 GCCTTTGAGCGTGCTCTAGCAGTCTATGACCAAGACACTCCGGACCGTTGGCACAATGTT

19 MetPheGluArgAlaLeuAlaValTyrAspLysAspThrProAspArgTrpHisAsnVal

295

28

59 GluAspLeulleAsn11eGluThrGlyArgValProLeuProAsnTyrLysThrPheGlu 78

39 AlarysAlaValGlyGlyLysThrValGluGluValLysArgHisTyrAspIleLeuVal

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ds; transcription factor; transgenic plant; growth rate; senescence; seed germination rate; plant vigor; seedling vigor.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant yield-related polynucleotide clone G1789.
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                                                                                                                                                                                                                                                                                                                                                ADD30327 standard; cDNA; 578 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001; 2001US-0310847P.
19-NOV-2001; 2001US-0336049P.
11-DEC-2001; 2001US-0338692P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana.
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Pilgrim ML,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to Arabidopsis thaliana nucleic acid sequences. The homologous or related genes, for producing compositions that modulate the capression or related genes, for producing compositions that modulate the regions of the protein, in diagnosis, for studying associated pathways, for genetic manipulation of cells, preferably planticells, in screening assays of various plant strains to determine the strains that are capable of withstending a particular disease or environmental stress, for enhancing or inhibiting production of biosynthetic products in plants and to create genetically modified and biosynthetic products in plants and to create genetically modified and crease useful for introducing or improving disease resistance and stress tolerance in plants, screening biologically active agents, such as tolerance in plants, screening biologically active agents, such as conjuncted and insecticides, and for elucidating biochemical pathways. Sequences ABX56649-ABX57647 represent Arabidopsis thaliana polynucleotides of the invention. Note: The sequence data for this patent of a plant of form part of the printed specification but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel Arabidopsis thaliana nucleic acid useful for identifying homologous or related genes, and to create genetically modified and transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          format directly from USPTO at segdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Price JL, Raines TM, Yu Y;
Ledford BL, Woessner JP, Haas WD;
Davis KR, Allen K, Hoffman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 556 BP; 146 A; 114 C; 115 G; 181 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organisms, such as plant cells and plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 473; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    An Y, Hamilton CM, P
Page A, Mathew AV,
Kricker M, Slater T,
                                                              26-JAN-2001; 2001US-00770152
                                                                                               27-JAN-2000; 2000US-0178503P
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286.00
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LEDFORD B L.
WOESSNER J P.
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RAMEAKA J G.
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RAINES T M.
                                                                                                                                                                                                                                                                                                                                  GARCIA C A.
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DAVIS K R.
ALLEN K.
HOFFMAN N.
                                                                                                                                GORLACH J.
                                                                                                                                                                                                                                                                                                                                                     KRICKER M.
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US2002040489-A1
                                                                                                                                                                                                                                                  PAGE A.
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Rameaka JG,
                                 34-APR-2002.
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(GARC/)
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(first entry)

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The invention relates to a number of isolated Arabidopsis thaliana CDNA sequences and their encoded proteins which are especially transcription factor related cDNA's and proteins. The isolated or recombinant plant transcription factor polynucleotides and polypeptides are useful in producing transgenic plants with commercially valuable properties, i.e. modified or altered desirable traits as compared to a reference plant, such as an alteration in a plant growth characteristic, e.g. growth rate, germination rate of seeds, vigor of plants and seedlings, or leaf and flower senescence. Sequence information related to the polynucleotides and polypeptides can also be used in bioinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the cDNAs of the invention.
                                                                                                                                                              New plant transcription factor polynucleotides and polypeptides, useful in producing transgenic plants with commercially valuable properties, such as an alteration in a plant growth characteristic, e.g. growth rate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 356; 454pp; English.
WPI; 2003-248221/24.
P-PSDB; ADD30328.
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1 MetalaSerAsnSerArgSerSerIle----SerProTrpThrPheSerGlnAsnLys 18

x ABX57121 (1-556)

US-10-697-787-2 (1-126)

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556 56 119 119

Matches: Conservative: Mismatches:

Indels:

Similarity:

Percent Similarity: Best Local Similarit

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Query Match:

Length:

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Heard JE;

n JL, Adam LJ, Dubell AT, Heard JE Reuber TL, Creelman RA, Pineda O,

Riechmann JL,

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GGAAACAGC 356
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     (PILG/)
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                                                                                                                                                                                                                                     38
                                                                                                                                                                                        28
                                                                                                                                                                                                                                                                                                                                                                                        transgenic; plant; enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone sensitivity; disease resistance; glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; flowering; flowering; flowering; flowering; flowering; flowering pattern; apical dominance; trichome; stem morphology; cot growth; root hair; seed development; cell proliferation; cell differentiation; premature senescence; necrosis; plant size; plant anthocyanin; light response; shade avoidance; bioinformatic; transcription factor; ds.
                                                                                                                                                                                                                         59 GluaspLeulleAsnileGluThrGlyArgValProLeuProAsnTyrLysThrPheGlu
                                                                                                              MetAlaSerAsnSerArgSerSerIle-----SerProTrpThrPheSerGlnAsnLys
                                                                                                                                                                                     39 AlaLysAlaValGlyGlyLysThrValGluGluValLysArgHisTyrAspIleLeuVal
                                                                                                                                                 19 MetPheGluArgAlaLeuAlaValTyrAspLysAspThrProAspArgTrpHisAsnVal
     BP; 188 A; 119 C; 117 G; 154 T; 0 U; 0 Other;
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                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                            US-10-697-787-2 (1-126) x ADD30327 (1-578)
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                               1.58e-27
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74.7%
67.5%
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HEARD J E.
HAAKE V.
CREELMAN R A.
RATCLIFFE O.
REUBER I L.
KEDDIE J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHERMAN B K.
RIECHMANN J
                                                                                                                                                                                                                                                             79 SerAsnSer
                                                Percent Similarity:
Best Local Similarity:
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     Sequence 578
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                     Alignment Scores:
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The invention describes a transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences fully defined in the specification or its complement. The method of the invention can be used to produced a plant having altered traits such as: enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; early or late flowering; altered flower structure, change in stem bifurcations, altered branching pattern, reduced apical dominance, reduced trichome density; lack of trichomes; reduced ectopic trichome development; altered trichome trichome colorens; increased root hairs; altered seed development; altered cell proliferation or cell differentiation; rapid development; altered cell proliferation or cell differentiation; rapid development; premanture seases in root anthocyanins; increase in seeding or plant size; decreased plant size; leaf morphology; seed biochemistry; increase in root anthocyanins; increase in plant cransgenic plant, polynucleotides and polypeptides are useful in bioinformatic search methods. This sequence represents a plant transgenic plant, polynucleotides and polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167
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                                                                                                                                                                                                                                                                                                                                                                                         New transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences, useful in bioinformatic search methods.
                                                                                                                                                                                                                  Broun PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetalaSerAsnSerArgSerSerIle----SerProTrpThrPheSerGlnAsnLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 AlaLysAlavalGlyGlyLysThrValGluGluValLysArgHisTyrAspIleLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluAspLeuIleAsnIleGluThrGlyArgValProLeuProAsnTyrLysThrPheGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 ATGGCATCAGGCTCAATGTCTTCTTATGGCTCTGGCTCATGGACTGTTAAGCAGAACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 MetPheGluArgAlaLeuAlaValTyrAspLysAspThrProAspArgTrpHisAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 GCCTTTGAGCGTGCTCTAGCAGTCTATGACCAAGACACTCCGGACCGTTGGCACAAGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 GCTAGAGCTGTTGGTGGTAAAACACCAGAAGAAGCTAAGAGACAGTATGACCTTCTAGTT
                                                                                                                                                                             Sherman BK, Riechmann JL, Jiang C, Heard JE, Haake V;
Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J,
Pilgrim ML, Dubell AN, Pineda O, Yu G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                578
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 578 BP; 188 A; 119 C; 117 G; 154 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 2719; 435pp; English.
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Matches:
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286.00
74.7%
67.5%
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BROUN P E.
PILGRIM M L.
DUBELL A N.
PINEDA O.
YU G.
                                                                                                                                                                                                                                                                                                  WPI; 2004-132245/13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                 P-PSDB; ADI44257
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This invention relates to novel isolated plant nucleic acid molecules, or variants thereof, that encode transcription factors. Specifically, it refers to transcription factor proteins that are cappalle of binding to DNA in order to regulate gene transcription and gene expression in a plants, in particular Eucalyptus grandis and Pinus radiata. The present invention describes DNA constructs containing DNA encoding a cranscription factor that regulates the promoter, which is operably linked to the desired mucleic acid to be expressed. It further provides transgenic plants expressing a transcription factor that confers a trait to the plant such as increased drought, salt or disease tolerance, height contritional characteristics, as well as improved taste, starch composition, flower longevity and germination, amongst others.

CC Accordingly, such plants that are successfully transfected with a DNA construct can be characterized by a difference in flower color, petal or leaf shape and size, aroma or plant height. This polynucleotide is a plant transcription factor cDNA sequence of the invention.
288 CGTGACATCGAAAGCATCGAGAATGGTCACGTGCCATTCCCTGACTACAAGACTACTACA 347
                                                                                                                                                                                                                                                                                                                                                               gene; 88; plant; transcription; gene regulation; gene expression;
transgenic plant; drought resistance; disease resistance; salt tolerance;
cold tolerance; freezing tolerance; flowering; flavor enhancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides isolated from plants encoding transcription factors, and polypeptides encoded by such polynucleotides, useful for regulating gene transcription and gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Connett MB, Emerson SJ, Frost MJ;
Higgins C, Lasham A, Lund ST, Magusin A;
Veerakone S, Westwood C, Gause K, Wood N
                                                                                                                                                                                                                                                                                                                       Eucalyptus grandis transcription factor cDNA MYB family Seq 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 482 BP; 137 A; 89 C; 121 G; 135 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  482
55
13
11
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; SEQ ID NO 306; 1265pp; English.
                                                                                                                                                                                             ADW16587 standard; cDNA; 482 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-2004; 2004WO-US017965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUN-2003; 2003US-0476189P
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285.00
84.0%
67.9%
                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bloksberg LN, Bryant C,
Forster RLS, Grigor M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Forster RLS, Grigor M,
Phillips J, Puthigae S,
                                                                                                             348 GGAAACAGC 356
                                                                  81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ARBO-) ARBORGEN LLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2005-075542/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eucalyptus grandis.
                                                                  79 SerAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    flower color.
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                                                                                                                                                                                                                                                                                   24-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JAN-2005
                                                                                                                                                                                                                                         ADW16587;
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⊗
                                                                                                                                                       RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New transgenic plants for producing commercially or agriculturally useful plants having improved tolerance to drought, shade and low nitrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 Arcicarcaccicarciritrargererecenteacheraccacacacacacaa 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 GCCTTTGAGCGTGCTCTAGCAGTCTATGACCAAGAGACACTCGGACCGTTGGCACAATGTT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to a novel plant transcription factor polypeptides, the DNA sequences which encode them and their use in creating transgenic plants. The transgenic plant and methods are useful for producing commercially or agriculturally useful plants having improved tolerance to drought, shade and low nitrogen conditions when compared to wild-type reference plants. The present sequence is that of a plant transcription factor gene which was used during the development of the transgenic plants of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 MetPheGluArgAlaLeuAlaValTyrAspLysAspThrProAspArgTrpHisAsnVal 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 AlaLysAlaValGlyGlyLysThrValGluGluVallysArgHisTyrAspIleLeuVal 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetAlaSerAsnSerArgSerSerIle-----SerProTrpThrPheSerGlnAsnLys 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluAspLeuIleAsnIleGluThrGlyArgValProLeuProAsnTyrLysThrPheGlu 78
                                                                                                                                                                             transcription factor; transgenic plant; agriculture; drought resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canales RD;
                                                                                                                                   Stress tolerant plant-related transcription factor gene SeqID875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Riechmann JL, Creelman RA, Ratcliffe OJ, Canales Kumimoto RW, Gutterson NI, Reuber TL, Pineda O; Morrison TA, Keddie JS, Jiang C, Century KS, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 578 BP; 188 A; 119 C; 117 G; 154 T; 0 U; 0 Other;
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56
6
19
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hearu ...,
Sheptti P, Kumimoto ..., Keddie
Sherman BK, Morrison TA, Keddie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MEND-) MENDEL BIOTECHNOLOGY INC.
        BP.
                                                                                                                                                                                                                                                                                                                                                                                                              13-NOV-2003; 2003US-00714887.
05-DEC-2003; 2003US-0527658P.
05-FEB-2004; 2004US-0542928P.
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286.00
74.7%
67.5%
      578
                                                                                                                                                                                                      stress tolerance; gene; ds
                                                                                         (first entry)
        standard; DNA;
                                                                                                                                                                                                                                           Arabidopsis thaliana
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Best Local Similarity:
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                                                                                         28-JUL-2005
                                                                                                                                                                                                                                                                                                                                26-MAY-2005
                                                AEA27034;
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990S-013532P.
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990S-0136392P.
990S-0137528P.
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990S-0137528P.
990S-0139453P.
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990S-0140833P.
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990S-0144331P.
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990S-0144331P.
990S-0144334P.
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99US-0145913P.
99US-0145918P.
18-MAY-1999;
19-MAY-1999;
20-MAY-1999;
21-MAY-1999;
25-MAY-1999;
27-MAY-1999;
20-JUN-1999;
04-JUN-1999;
04-JUN-1999;
06-JUN-1999;
08-JUN-1999;
10-JUN-1999;
110-JUN-1999;
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22 - 70N - 1999)
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15-70L-1999;
16-70L-1999;
19-70L-1999;
19-70L-1999;
19-70L-1999;
19-70L-1999;
20-70L-1999;
20-70L-1999;
21-70L-1999;
21-70L-1999;
21-70L-1999;
22-70L-1999;
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24-JUN-1999;
28-JUN-1999;
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16-JUN-1999;
17-JUN-1999;
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 156
                                                                                                                          216
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                                                                                                                                        40
                                                                                                         9
                                                                                                                                                                                                                                                                                                      Hybridisation assay, genetic mapping; gene expression control, protein identification; signal transduction pathway; metabolic pathway; promoter, termination sequence; ss.
                                                                 MetAlaSerAsnSerArgSerSerIleSerProTrpThrPheSerGlnAsnLysMetPhe
                                                                                                      AlaValGlyGlyLysThrValGluGluValLysArgHisTyrAspIleLeuValGluAsp
                                                                                                                                                                                                                                                                                      Arabidopsis thaliana DNA fragment SEQ ID NO: 62553.
Gaps:
                US-10-697-787-2 (1-126) x ADW16587 (1-482)
                                                                                                                                                                                                                                  AAC49819 standard; DNA; 504 BP
                                                                                                                                                                                                                                                                                                                                                                                                                 990S-0121825P.
990S-0123180P.
990S-0125788P.
990S-012664P.
990S-01267824P.
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990S-0132486P.
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990S-0132486P.
990S-0132486P.
990S-0132486P.
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                                                                                                                                                                                                                                                                     18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
                                                                                                                                                                                              274 AGC 276
                                                                                                                                                                              Ser 81
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05-MAR-1999;
22-MAR-1999;
25-MAR-1999;
26-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
16-APR-1999;
19-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
30-APR-1999;
30-APR-1999;
30-APR-1999;
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06-MAY-1999;
07-MAY-1999;
07-MAY-1999;
11-MAY-1999;
14-MAY-1999;
14-MAY-1999;
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                                                                                                       41
                                                                                                                        157
                                                                                                                                                                                                                                                   AAC49819;
                                                                                                                                                                             81
                                                                                                                                                                                                                 RESULT 14
                                                                                                                                                                                                                          AAC4981
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Same Same

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PR 27-7UL-1999; 99US-0145319P.
PR 02-AUG-1999; 99US-014638P.
PR 02-AUG-1999; 99US-014638P.
PR 02-AUG-1999; 99US-014638P.
PR 03-AUG-1999; 99US-014638P.
PR 04-AUG-1999; 99US-0147132P.
PR 04-AUG-1999; 99US-0147132P.
PR 05-AUG-1999; 99US-0147132P.
PR 05-AUG-1999; 99US-0147132P.
PR 13-AUG-1999; 99US-014743P.
PR 23-AUG-1999; 99US-01493EP.
PR 23-AUG-1999; 99US-01536EP.
PR 23-AUG-1999; 99US-01536EP.
PR 23-AUG-1999; 99US-01536EP.
PR 23-AUG-1999; 99US-01536EP.
PR 24-EEP-1999; 99US-01536EP.
PR 25-EEP-1999; 99US-01593EP.
PR 25-EEP-1999; 99US-01593EP.
PR 26-CCT-1999; 99US-01593EP.
PR 26-CCT-1999; 99US-01593EP.
PR 21-CCT-1999; 99US-01692EP.
PR 21-CCT-1999; 99US-01692EP.
PR 21-CCT-1999; 99US-01693EP.
P
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Plant; gene; ss; transcription; plant genome augmentation; cereal; soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet; maize; bartley; soorghum; rice; wheat; crop plant; insecticide resistance; stress tolerance; salt tolerance; cold tolerance; drought tolerance; plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
                                                                                                                                                                                                                                                                                                           162
                                                                                                                                                                                                                21 GluargalaLeualaValTyraspLysAspThrProAspArgTrpHisAsnValAlaLys 40
                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                             preulleAsnileGluThrGlyArgValProLeuProAsnTyrLysThr-PheGluSerA 80
                                                                                                                                                                                                                                                                                                                                  snSerArgSerIle-AsnAspPheAspThrArgTyrIleThrLysTyrLeuTyrMetMet 99
                                                                                                                                                                                                                                                       AlavalGlyGlyLysThrValGluGluValLysArgHisTyrAsp-11eLeuValGluAs
                                                                                                                                                                           MetalaSerAsnSerArgSerSer11eSerProTrpThrPheSerGlnAsnLysMetPhe
                                                                                                                                                                                      LeuSerIleTyrPheAspAsnHisSerSerAspPheGluLys 113
                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
Gaps:
                                                                                       Length:
Matches:
                                                                                                                                                          US-10-697-787-2 (1-126) x AAC49819 (1-504)
99US-0161359P.
99US-016136DP.
99US-0161361P.
99US-0161992P.
99US-0161991P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-SEP-2001; 2001US-0325277P.
26-SEP-2001; 2001US-0325448P.
04-APR-2002; 2002US-0370620P.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADJ43786 standard; cDNA; 466
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                                                                                    1.69e-26
277.50
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26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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                                                                              Alignment Scores:
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New rice promoter, useful for manipulating crop plants to alter or improve phenotypic characteristics, e.g. produce large quantities of oil or proteins, resistance to insecticides, virus or fungi, stress tolerance or high nutritional value.
                                                                                 T, Briggs SP, Cooper B, Glazebrook J;
Kreps J, Provart N, Ricke D, Zhu T;
                                                                                                                                                              Example 13; SEQ ID NO 4786; 230pp; English.
                                                                                 Moughamer T,
BRIGGS S P.
COOPER B.
GLAZEBROOK J.
                                                                                         Katagiri F,
                       GOFF S A.
KATACIRI F.
KREPS J.
PROVART N.
RICKE D.
                                                                                                         WPI; 2004-190374/18
                                                                                 Budworth P,
                                                                                         Goff SA,
                              (KATA/) F
(KREP/) F
(PROV/) E
(RICK/) F
(ZHUT/) 2
(BRIG/)
(COOP/)
(GLAZ/)
(GOFF/)
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The invention relates to plant nucleotide sequences that direct seed...

leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential

or constitutive transcription of an operatively linked nucleic acid

segment. The invention also relates to a method for augmenting a plant

segment and a method of identifying a gene, where its expression is

clatered in the seed, leaf, stem, panicle, pollen, root or is constitutive

clanda, cotton, peanut, tobacco or sugar beet, preferably maize, barley,

canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,

canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,

canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,

corghum, rice or wheat. The polymucleotides and the polypeptides they

cencede are useful for manipulating crop plants to alter or improve

phenotypic characteristics, to produce large quantities of oil or

contents, to incur resistance to insecticides, viruses or improve

contents, to incur resistance to insecticides, viruses or fungi, and to

incur stress tolerance (e.g. salt, cold or drought) to ensure the plants

content and nutritional value with reduced apical dominance or dwarfism,

can incur stress tolerance (e.g. salt, reduced apical dominance or dwarfism,

can incur stress tolerance (e.g. salt, reduced apical dominance or dwarfism,

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can incur stress tolerance (e.g. salt, reduced apical dominance or dwarfism,

can incur stress tolerance (e.g. salt, redu Sequence 466 BP; 93 A; 127 C; 124 G; 122 T; 0 U; 0 Other; Length:
Matches:
Conservative:
Mismatches: 2.38e-26 276.00 60.0% 47.1% 42.18 Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB:

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                                                                                                                                                                                                                                                                                                                191 GGATGAAGTGTCGACTGGATCAAAAGTGTAGAAACGGGCAGCAG-TCTACTCTGGATGAT 133
                                                                                             21 GluArgAlaLeuAlaValTyrAspLysAspThrProAspArgTrpHisAsnValAlaLys 40
                                                                                                                                                           41 AlaValGlyGlyLysThrValGluGluValLysArgHisTyrAspIleLeuValGluAsp 60
                                                                                                                                                                                                                                                                                             ------LysThrPheGluSerAsgSerIleAsnAspPhe 87
                                MetAlaSerAsnSerArgSerSerIleSerProTrpThrPheSerGlnAsnLysMetPhe
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US-10-697-787-2 (1-126) x ADJ43786 (1-466)
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Search completed: March 10, 2006, 19:27:24 Job time : 480 secs This Page Blank (uspto)

us-10-697-787-2.p2n.rge

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - nu	OM protein - nucleic search, using Grame plus pan model
Run on:	<pre>March 10, 2006, 19:17:45 ; Search time 3944 Seconds (without alignments) 1815.993 Million cell updates/sec</pre>
Title: Perfect score: Sequence:	US-10-697-787-2 656 1 MASNSRSSISFWTFSQNKMFHSSDFEKFSQKVLVSXISLV 126
Scoring table:	BLOSUM62 Xgapop 10.0 , Xgapext 0.5 Ygapop 10.0 , Ygapext 0.5 Fgapop 6.0 , Fgapext 7.0 Polop 6.0 , Fgapext 7.0

11766282 Total number of hits satisfying chosen parameters:

5883141 segs, 28421725653 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

4.		
	Description	AYS19525 Arabidops AC025814 Arabidops CS138004 Sequence
SUMMARIES	No. Score Match Length DB ID	15 AYS19525 15 AC025814 6 CS138004
	98	15
	Length	381 1 68041 1 294 6
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	No. Score Match Length DB IL	656 656 473
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RESULT 1			
AY519525			
LOCUS	AY519525		
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ALIGNMENTS

linear PLN 07-FEB-2004 Arabidopsis thaliana MYB transcription factor (At1g75250) mRNA, complete cds. LOCUS DEFINITION

AY519525 AY519525.1 GI:41618977 VERSION KEYWORDS SOURCE ORGANISM ACCESSION

REFERENCE AUTHORS TITLE

Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukarota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases I to 381)
S Qu,L. and Gu,H.
S The WTB Transcription Factor Family in Arabidopsis: A Genome-Wide Cloning and Expression Pattern Analysis
L Unpublished
L Unpublished
L Unpublished
S (bases I to 381)
S Qu,L. and Gu,H.
Birct Submission
L Submission
Submitted (07-JAN-2004) Life Sciences, National Laboratory of Submitted (07-JAN-2004) Life Sciences, National Laboratory of Protein Engineering and Plant Genetic Engineering, Peking University, Beijing 100871. China JOURNAL REFERENCE AUTHORS TITLE JOURNAL

.381
 /organism="Arabidopsis thaliana"

FEATURES

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crouse were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, http://CR-081.mt.edu/GENSCAN.html), GeneMarkHym (Mark Borodovsky, http://Genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant of GlimmerM, see Mihaela Pertea, http://www.rigr.org/scflab/glimmerm.htm/glimmerA.html, and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without proteins over medt of their length are annotated as hypothetical proteins Genes encoding tRNAs are predicted by transcriber similarity, the are predicted by more than two gene prediction proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.washington.edu/RM/RepeatMasker.html).

Simple repeats are identified by repeatmasker (Arian) Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html).
                                    Direct Submitted (15-MR2-2000) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA, xlin@tigr.org a (bases 1 to 68041)

Submitted (12-SED-2000) The Institute for Genomic Research, 9712 Submitted (12-SED-2000) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org 1 to 68041)

S Town, C.D. and Kaul, S. Direct Submission

Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org Nedical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org E (Dases 1 to 68041)

S Town, C.D. and Kaul, S. Direct Submission

L Submitted (12-OCT-2000) The Institute for Genomic Research, 9712

Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org

S Town, C.D. and Kaul, S. Direct Submission

L Submitted (12-OCT-2000) The Institute for Genomic Research, 9712
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Rnengathlyqvpatmegpiptovvdnysllukieskstpipavekklpcnegreevk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BAC clone F22H5 is from Arabidopsis thaliana chromosome 1
The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                      Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org 6 (bases 1 to 68041)
Town,C.D. PhD.
Direct Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (22-JAN-2001)
On Jan 22, 2001 this sequence version replaced gi:12280794
Address all correspondence to:at@tigr.org
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/product="unknown_protein, 3'
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                                                      AC025814 68041 bp DNA linear PLN 22-JAN-2001
Arabidopsis thaliana chromosome 1 BAC F22H5 genomic sequence,
complete sequence.
AC025814, 7 GI:12331602
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 68041)
Lin,X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B.J.,
Mu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R.,
Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
Arabidopsis thaliana chromosome I BAC F22H5 genomic sequence
2 (bases I to 68041)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetAlaSerAsnSerArgSerSerIleSerProTrpThrPheSerGlnAsnLysMetPhe
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AUTHORS
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complement (join(<16410. .16558,16703. .16830,17050. .>18554))
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complement (16410. .18554)
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oxidoreductase, putative; 14094-12769"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerArgSerIleAsnAspPheAspThrArgTyrIleThrLysTyrLeuTyrMetMetLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21255 TCGATATATTTTGATAATCATTCTAGTGATTTTTGAGAAATTCTCTCAAAAGTTCTTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluArgAlaLeuAlaValTyrAspLysAspThrProAspArgTrpHisAsnValAlaLys
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                                                                                                                                                                                              /gene="F22H5.1"
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Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Nayven, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A. Arabidopsis Open Reading Frame (ORF) Clones

Unpublished

2 (bases 1 to 334)
2 (bases 1 to 334)
3 Yamada, K., Chan, M., Chang, C.H., Dale, J.M., Mong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Niguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.

Direct Submission

AL Submitted (15-AMR-2003) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAs (RAFL CDNAs 'RIKEN Arabidopsis Full-Length CDNA'): Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Ishida, J., Sakurai, Y. and Shinozaki, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.
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Location/Qualifiers
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7
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/note="This clone is in pUNI 51."
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Matches:
Conservative:
Mismatches:
Indels:
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| Mol. Lype="mRNA"
| db_xref="taxon:3702"
| /chromosome="1"
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Query Match:
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Arabidopsis thaliana clone U51233 putative myb family transcription factor (At1919510) mRNA, complete cds.
                                                                                                     PAT 09-AUG-2005
                                                                                                                                                                                                               Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantaes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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(bases 1 to 334)
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Onodera,C.S., Quach,H.L., Tang,C., Toriumi,M., Wong,C., Wu,H.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGAGGGCCTTGGCAGTTTACGACAAGGACACCCCGACGATGGCAAATGTGGCAAAA 120
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Patent: WO 2005047516-A 975 26-MAX-2005;
Mendel Biotechnology, Inc. (US)
Location/Qualiflers
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                21315 AGTTATATTTCTTTGGTT 21332
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An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al. (1998) Plant J. 15:707-720; Seki et al. (2002) Science 296:141-145). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1-E vector (Carninci et al. (2001) Genomics 77:79-90) digested with BamHI and Sall. This clone is in a modified pBluescript vector.

Please visit our web site (http://pfgweb.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AK119034 580 bp mRNA linear PLN 14-FEB-2004 stabidopsis thaliana At1g19510 mRNA for putative myb-related protein, complete cds, clone: RAFL21-36-F10.
AK119034
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FLI CDNA; CAP trapper.
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Arabidopsis thaliana (thale burnatura)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliara full-length cDNA
Published Only in Database (2002)
2 (bases 1 to 580)
Seki, M., Iida, K., Satou, M., Sakurai, T., Akiyama, K., Ishida, J., Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Carninci, P., Direct Submission
                                                                                                                                                                                                                                                                                          SerAsnSerArgSerIleAsnAspPheAspThrArgTyrIleThrLysTyr----
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268 CTCATGAACATCGAACAAGACTTAGTACCTTTGCCTAAATACAAAACCGTCGATGTTGGA 327
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Qu,L. and Gu,H.

The MYB Transcription Factor Family in Arabidopsis: A Genome-Wide Unpublished
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1. .303
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Submitted (07-JAN-2004) Life Sciences,
Protein Engineering and Plant Genetic E
University, Beijing 100871, China
Location/Qualifiers
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Qu, L. and Gu, H.
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Submitted (22-APR-2000) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th Street and
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
4 (bases 1 to 12097)
S Cheuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, O.,
Choi, E., Conn, L., Comway, A., Gonzalez, A., Hansen, N.,
Inu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H.,
Schwartz, J., Southwick, A., Thaveri, A., Troitumi, M., Vaysberg, M.,
Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.
Direct Submission
AL Submitted (18-10N-2000) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th and
Hamilton Walk, Philadelphia, PA 19104-6018, USA
S (bases 1 to 12097)
S (bases 1 to 12097)
Conway, A., Gonzalez, A., Hansen, N., Howings, N., Mukharsky, N.,
Lenz, C., Li, J., Liu, A., Liu, J., Liu, S., Mukharsky, N.,
Direct Submission
Submitted (11-OCT-2000) Arabidopsis thaliana Genome Center,
Doatoway, R., Philadelphia, PA 19104-6018, USA
On Apr 22, 2000 this sequence version replaced gi:7543634.
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DDSESDDDVVAKPIFCSRRAVHVAMTLDAA\IRGSVAAVLSVLQHSSGPENIYPHFVA
SASADASSLAATISSSFYLDFTVYYFNVSSVSRLISSSIRSALDCPLNYARSYLADL
LPPCVRRVVYLDSDLILVDDIAKLAATDLGRDSVLLAPEYCNANFTGYFTSTFMSNPT
LSLFPADRKACYPTGWYIDLSKRREGAYTSRIESMWAMQKRMRIYELFSFFLLV
FAGLIKPVNHRWNQHGLGGDNFRGLCRDLHPGPVSLLHWSGKGKPWARLDAGRPCPLD
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/note="similar to Zn finger protein gi|6319911"
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/db_xref="taxon:3702"
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/evidence=not_experimental
/product="F18014.1"
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90. .2159
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AC025808 GI:7636235
                                                   | locus tag="At1g19510"
| codon_start=1
| product="MYB transcription factor"
| protein_id="AAS0994.1"
| db_xref="G1:418974"
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1 (Dases 1 to 12097)
Shinn, P., Brooks, S., Buehler, E., Chao, Q., Johnson-Hopson, C., Khan, S., Kam, C., Altafi, H., Bei, Q., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzales, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Ler, C., Li, J., Liu, A., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaologis, A. and Ecker, J. R.

Federspiel, N. A., Theologis, A. and Ecker, J. R.

Genomic sequence for Arabidopsis thaliana BAC F18014 from
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/trānslation="WAGRRDRSQQLRGSRIAIAILIGIFIGCVCAVLFPYGFFNSSSS LKASBELKSSKOVVSSSACESPERVKMLKSDFYTLSEKNBELKKQVRELTEKLRLAEQ
GSDNARKQVLALGTQIKAGPFGTVKSLRTNPTILPDESINPRLAKILEEIAVDKEVIV
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GKTGGNHAVSGLKFRVLREFLQLGYGVLLSDVDIVFLQNPFSHLYRDSDVESNSDGHD
                                                                                                                                                                         NHTAYGENDUFDEPANGWARYAHTMINVENGGEFULRETIPSIELLORVARELSKAK
WMOQAVFNEELFYESHPEYTALHASKRVMOMYEFNASKVLFKTVRKNHELKKKVKPVI
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/note="unknown protein; similar to ESTs gb | T42717.1,
emb | F13886.1, and emb | F13885.1"
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/evidence=not experimental
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VSVSETNREAVLLHNLEELVKNLTELVANLDAKLSATPLKEKNBISVDDDIGEEKERG
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WNSNSVSMEHVGKFDVDDSADPVTLLEVHHVGRVRYILATDLSGKLTVLTENRTVYGS
VIPSSRPLVFLKQRLLFLTESGAGSLDLRSMKIRETECEGLNHSLARTYVFDAAERSK
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Wiridiplantae; Streptophyta; Core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 5443)
1 (bases I to 5443)
Barnstead,M.E., Mason,T.M., Bowman,C.L., Ronning,C.M.,
Benito,M.-I., Carrera,A.J., Creasy,T.H., Buell,C.R., Town,C.D.,
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       쉽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Join(17994. 18489,18568. 18698,18814. 18847,19006. 19099,
19170. 19347,19441. 19479,19616. 19715,19855. 19994)
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GFPDAAMYGAAASGGFPHGFSNPFHGGHSHWHSYQRHTGRQGQDHHLRILLLIVFVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HFQDSRYFLKV"

join(22037. .22300,22618. .23361)

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dbj|AV440785.1"
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90367

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40

90307

78

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                                                                                                                                                                                                                                                                                                                                                                                                                                               GVGYNKPISGGRRGETSIRGGHAGERRISDVTHINCRFHEYRSLPSNKMARCRAAAGV
IDGKIYVIGGRKSWSSVPGPYPEAFGRGEFLTYANMEKIYCLDLTRNIHIYDPKESK
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SWYILHRKPYRNLPNTISLKLCKIDSLPPMPMGSTVVTIGSDIYVLGGRANGEKLLEDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /trānslation="MATNVEYTCFVRGLDQDTDEKDLTDIFSKFGNVIDSKIIYDRDT
GKSRRFGFVTFEEEKSMTDAIMIMDVEESRSKCVNVGSITVEVARQRRKNRSAEFALB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="symonym: F2G1.4; Alternative splicing exists based on EST evidence, form 1 splice site is AG, form 2 splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt family="Rf:182A repeat X93610, similar to genes encoding glycine-rich proteins e.g., CCR2, L04172; GRP7, Z14987, 20 copies#Rf:ATR0048|X93610 182A"
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9099. 9179
/gene="At2g21670"
9099. 9179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (9910, 9934)
/rpt family="(TAG)n"
10224, 10311
                                                                                     /gene="At2g21680"
/note="avre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="(CGG)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="At2g21655"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9099. .9179
/gene="At2g21670"
                                                                       LVRLINEKQKKMAGL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="At2g21660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ceres: 10836"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           site is
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               Direct Submission

Direct Submission

Direct Submission

Medical Center Dr., Rockville, MD 20850, USA

Medical Center Dr., Rockville, MD 20850, USA

S Submitted (99-MAR-2000) The Institute for Genomic Research, 9712

Town,C.D. and Kaul,S.

Direct Submission

N. Submitted (27-FEB-2002) The Institute for Genomic Research, 9712

Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org

On Apr 18, 2002 this sequence version replaced gi:6598668.

Sequencing, analysis, and annotation were performed within the CSHL/WUSC/ABI Arabidopsis Genome Sequencing Consortium.

Information on physical mapping and YAC and BAC library construction as well as added annotation can be viewed at http://www.cshl.org/arabweb/. We used GenScan, Grail, and MZEF for predicting coding exons and assembling genes. BAC F6F23 maps to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EBVGRLLLAYRPHLMGGSIEERWRPLVKYFYYLGIPKEGMKRILLVVKPILYCIDLEKTI
APKVVELRYNVRFLOEMGIPNEAIGMLVKPPSLLTNGLYKKIRVPIPLLTRAGYTOK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RWIKHHELSYNRIAKIICMSKGNLDSIRIMIEWLKSIHVKGEFIAVAFLRSGDNILQR
NREELNEIVEYUSYLESNGVRRDWMGYVVGRCPELLSFSMEEVKSRVDFFLKMGMNQNDFG
TMVYDYPKIIGFFSFQVMEKKVLKALFNTPALRLSFKFIIVLLVLNQINYLKEFGLST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="33956 bases before this point were not included in the submitted ssequence, due to overlap with another BAC" complement (2681. .5102)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /ecotype="Columbia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERRVRDKVERRERFEAGLDSEDSQPSDENISDQEIAFSDEAEEEDLTE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. 54433"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5254. .5325
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5254. .5325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5391. .5874
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(bases 1 to 54433)
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84802
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                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
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                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (13-MAY-2005) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA ON May 13, 2005 this sequence version replaced gi:59933338.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (18-FEB-2005) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
3 (Dases 1 to 108844)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LeulleAsnileGluThrGlyArgValProLeuProAsnTyrLysThrPheGluSerAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 SerArgSerIleAsnAspPheAspThrArgTyr-----IleThrLysTyrLeuTyr
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                                                                                                                                                                               Town, C.D., Tallon, L.J., Arbogast, T., Althoff, R., Hine, E., Monaghan, E., Smith, S.A., Utterback, T., Feldblyum, T., Koo, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 TyrPheAspAsnHisSer------SerAspPheGluLys 113
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23
24
28
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Matches:
Conservative:
Mismatches:
Indels:
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Unpublished
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Medicago truncatula
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                  GI:63987073
                                                                                                                                           Medicago.
1 (bases 1 to 108844)
                                                                                                                                                                                                                                                                        (bases 1 to 108844)
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293.00
61.8%
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 AC157502
AC157502.2
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16334 ATGGCATCAGGCTCAATGTCTTCTTATGGCTCTGGCTCATGGACTGTTAAGCAGAACAAA 16275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16214 GCCTTTGAGCGTGCTCTTAGCAGTCTATGACCAGACACTCCGGACCGTTGGCAATGTT 16215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC157502 108844 bp DNA linear PLN 13-MAY-2005 Medicago truncatula chromosome 7 BAC clone mtel-56e23, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 GluAspLeuIleAsnIleGluThrGlyArgValProLeuProAsnTyrLysThrPheGlu 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 MetPheGluArgAlaLeuAlaValTyrAspLysAspThrProAspArgTrpHisAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 AlaLysAlaValGlyGlyLysThrValGluGluValLysArgHisTyrAsplleLeuVal
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Matches:
Conservative:
Mismatches:
Indels:
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complement (15427. 16406)
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296.00
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AC157502
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                                                                                                                     Cheuk, R., Chen, H., Kim, C.J., Shinn, P. and Ecker, J.R.
Arabidopsis cDNA clones
Unpublished
(Dases 1 to 506)
Cheuk, R., Chen, H., Kim, C.J., Shinn, P. and Ecker, J.R.
Cheuk, R., Chen, H., Kim, C.J., Shinn, P. and Ecker, J.R.
Direct Submission
Submitted (29-NOV-2003) Salk Institute Genomic Analysis Laboratory (SIGMAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 GAAAGGGCGTTGGCTACATATGACCAGGACACTCCTGACGTTGGCATAACGTTGCAAGA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 GluargalaLeualavalTyraspLysaspThrProAspArgTrpHisAsnValAlaLys 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 AlavalGlyGlyLysThrValGluGluValLysArgHisTyrAspIleLeuValGluAsp 60
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51
16
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/organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              51"
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /ecotype="Columbia"
/note="This clone is in pUNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                  FLI CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="unknown protein"
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AY519526.1 GI:41618981
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 BT010770.1
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                                                                                                                                                                                                                                                                   Unpublished

2 (bases 1 to 246)

2 (bases 1 to 246)

Direct Submission

Submitted (14-JAN-2004) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
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                                      PLN 14-JAN-2004
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1 (bases 1 to 246)
Cheuk, R., Chen, H., Kim, C.J., Shinn, P. and Ecker, J.R.
Arabidopsis ORF clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LeulleAsnileGluThrGlyArgValProLeuProAsnTyrLysThrPheGluSerAsn 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGCTTCCAACTCAATGAGCTCTAGCGCTTCTTGGACACGTAAGGAGAACAAATTATTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 GluArgAlaLeuAlaValTyrAspLysAspThrProAspArgTrpHisAsnValAlaLys 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 AlavalGlyGlyLysThrValGluGluValLysArgHisTyrAspIleLeuValGluAsp 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetAlaSerAsnSerArgSerSerIleSerProTrpThrPheSerGlnAsnLysMetPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BT010770 506 bp mRNA linear Arabidopsis thaliana At4g36570 mRNA, complete cds. BT010770
                                      BT011255 246 bp mRNA linear Arabidopsis thaliana At4g36570 gene, complete cds.
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51
16
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Arabidopsis thaliana"
/mol type="mRNA"
/db_xref="taxon:3702"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /ecotype="Columbia"
/note="This clone is in pUNI 51"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                        FLI CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .246
/note="unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-697-787-2 (1-126) x BT011255 (1-246)
                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="C62918"
                                                                                        BT011255.1 GI:40823587
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289.00
83.8%
63.8%
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Best Local Similarity:
Query Match:
DB:
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BT010770
LOCUS
DEFINITION
ACCESSION
                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                  BT011255
LOCUS
DEFINITION
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                                                                                                                                                                                                             REFERENCE
AUTHORS
TITLE
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AUTHORS
TITLE
JOURNAL
   RESULT 10
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74.7%
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Pred. No.:
                  REFERENCE
AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                             COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                       /protein id="AaS09996.1"
| Dax xxef="01:41618982"
| translation="WASGSWGSYGSGSWTVKQNKAFERALAVYDQDFBDRWHNVARAV
| GGKTPEEAKRQYDLLVRDIESIENGHVPFPDYKTTTGNSNRGRLRDEEKRMRSMKLQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana clone U50297 putative myb family transcription Brooss4
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GCCTTTGAGCGTGCTCTAGCAGTCTATGACCAAGACACTCCGGACCGTTGGCACAATGTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                                          1 (bases 1 to 306)
Qu.L. and Gu.H.
The MYB Transcription Factor Family in Arabidopsis: A Genome-Wide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MetalaSerAsnSerArgSerSerIle----SerProTrpThrPheSerGlnAsnLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 AlaLysAlaValGlyGlyLysThrValGluGluValLysArgHisTyrAspIleLeuVal
                                                                                                                        2 (bases 1 to 306)

Qu,L. and Gu,H.

Direct Submission
Submitsed (07-JAN-2004) Life Sciences, National Laboratory
Protein Engineering and Plant Genetic Engineering, Peking
University, Beijing 100871, China
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/product="MYB transcription factor"
                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                      /locus_tag="At2g21650"
|. .306
                                                                                                                                                                                                                                                                                                                                                          /locus_tag="At2g21650"
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286.00
74.7%
67.5%
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                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
                                                            AUTHORS
TITLE
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AUTHORS
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JOURNAL
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BT008554
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Dipublished

Yamada,K., Dale,J.M., Hsuan,V.W., Onodera,C.S., Quach,H.L.,

Yamada,K., Dale,J.M., Hsuan,V.W., Onodera,C.S., Quach,H.L.,

Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Carninci,P., Chen,H.,

Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Kawai,J.,

Kim,C.J., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M.,

Saki,M., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K.,

Davis,R.W., Ecker,J.R. and Theologis,A.

Direct Submission

L. Submitted (16-MAY-2003) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 337)
Yamada.K., Dale,J.M., Hsuan,V.W., Onodera,C.S., Quach,H.L.,
Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Carninci,P., Chen,H.,
Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Kawai,J.,
Kim,C.J., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M.,
Seki,M., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K.,
Davis,R.W., Ecker,J.R. and Theologis,A.
Arabidopsis Open Reading Frame (ORF) Clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MASGSMSSYGSGSWTVKQNKAFERALAVYDODTPDRWHNVARAV
GGKTPEEAKRQYDLLVRDIESIENGHVPFPDYKTTTGNSNRGRLRDEEKRMRSMKLQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada.K., Dalle,J.W., Hsuan,V.W., Onodera,C.S., Quach,H.L., Toriuni,M., Wong,C., Wu,H.C., Yu,G.,Y., Van,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Annotation based on July 2002 version of the Arabidopsis genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=experimental
product="putative myb family transcription factor"
/protein id="AR40181.1"
/db_xref="GI:30793857"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to this work. Shinozaki, K. (RIKEN GSC) and Thee /PGEC) contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            337
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6
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2
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/chromosome="2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
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/note="This clone is in pUNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to Genbank.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307. .337
/gene="At2g21650"
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/trānslation="masgsmssygsgswtvkqnkaferalavydqdfpdrwhnvarav
ggktpeeakrqydllvrdiesienghvpfpdyktttgnsnrgrlrdeekrmrsmklq"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAT 09-AUG-2005
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                                                                                                                                                                                                                                                                                            /ecotype="Columbia"
/note="This clone is in a modified pBluescript vector2
(lambda PS) as a BamHI/XhoI insert."
Annotation based on July 2002 version of the Arabidopsis genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaLysAlaValGlyGlyLysThrValGluGluValLysArgHisTyrAspIleLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetAlaSerAsnSerArgSerSerIle----SerProTrpThrPheSerGlnAsnLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=experimental
/product="putative myb family transcription factor"
/protein id="Ap40504.1"
/db_xref="GI:30794124"
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/note="not present in genomic sequence"
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/replace="g"
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                             /organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                             (R50297) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         578 bp DNA WO2005047516.
                                                                                                                                                                                                                                                             /clone="RAFL17-18-C23
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                                                      Location/Qualifiers
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Yamada, K., Dale, J.M., Hsuan, V.W., Onodera, C.S., Quach, H.L.,
Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H.,
Toriumi, M., Wong, C., Wu, H.C., Jones, T., Kamiya, A., Kawai, J.,
Kim, C.J., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Sarou, M.,
Saki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K.,
Davis, R.W., Ecker, J.R. and Theologis, A.
Direct Submission
L. Submitted (16-MAY-2003) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the
Collection and Clustering of KNFL cDNAs (RAFL cDNA: RIKEN
Arabidopsis Full-Length cDNA'): Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryocta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 570)
Yamada, K., Dale, J.M., Heuan, V.W., Onodera, C.S., Quach, H., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Kim, C.J., Narusaka, M., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Yaguyen, M., Palm, C.J., Sakurai, T., Sarou, M., Seki, M., Ecker, J.R. and Theologis, A. Tripp, M.G., Wu, T., Shinozaki, K., Labidopsis Full Length CDNA Clones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BT008698 Arabidopsis thaliana clone RAFL17-18-C23 (R50297) putative myb family transcription factor (At2g21650) mRNA, complete cds.
                                                                                                                                                                                                                                                             The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada,K., Dale,J.M., Hisuan,V.W., Onodera,C.S., Quach,H.L., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Chen,H., Cheuk,R., Jones,T., Xim,C.J., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Davis,R.W., Ecker,J.R. and Theologis,A.
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                Heard, J.E.
Plant transcriptional regulators
Plant transcriptional regulators
Learent: WO 2005047516-A 875 26-MAY-2005;
Mendel Biotechnology, Inc. (US)
Location/Qualifiers
i. corganism="Arabidopsis thaliana"
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